

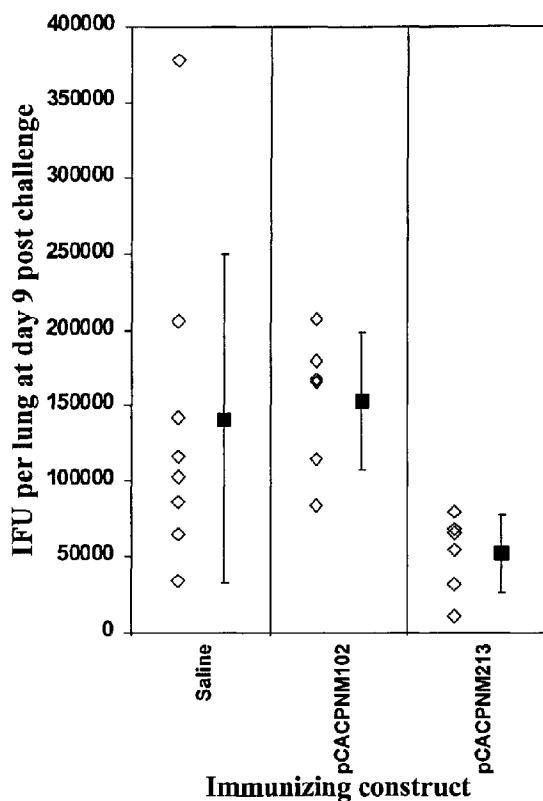
(19) World Intellectual Property Organization  
International Bureau(43) International Publication Date  
15 November 2001 (15.11.2001)

PCT

(10) International Publication Number  
**WO 01/85972 A2**

- (51) International Patent Classification<sup>7</sup>: **C12N 15/85**, 60/235,361 26 September 2000 (26.09.2000) US  
A61K 48/00, C07K 19/00, 16/12, A61K 39/118, 39/40 60/235,398 26 September 2000 (26.09.2000) US
- (21) International Application Number: PCT/CA01/00653 (71) Applicant (for all designated States except US): **AVENTIS PASTEUR LIMITED** [CA/CA]; Connaught Campus, 1755 Steeles Avenue West, Toronto, Ontario M2R 3T4 (CA).
- (22) International Filing Date: 8 May 2001 (08.05.2001)
- (25) Filing Language: English
- (26) Publication Language: English
- (72) Inventors; and  
(75) Inventors/Applicants (for US only): **MURDIN, Andrew, D.** [GB/CA]; 11 Forest Hill Drive, Richmond Hill, Ontario L4B 3C2 (CA). **OOMEN, Raymond, P.** [CA/CA]; 29 Kennedy St. W., Aurora, Ontario L4G 2L6 (CA). **WANG, Joe** [CA/CA]; 51 Aspenwood Drive, Toronto, Ontario M2H 2E8 (CA). **DUNN, Pamela** [GB/CA]; 97 Rosebury Lane, Woodbridge, Ontario L4L 3Z1 (CA).
- (30) Priority Data:  
60/202,672 8 May 2000 (08.05.2000) US  
60/207,852 30 May 2000 (30.05.2000) US  
60/211,801 16 June 2000 (16.06.2000) US  
60/212,044 16 June 2000 (16.06.2000) US  
60/211,797 16 June 2000 (16.06.2000) US  
60/211,796 16 June 2000 (16.06.2000) US  
60/211,798 16 June 2000 (16.06.2000) US  
60/235,335 26 September 2000 (26.09.2000) US
- (74) Agents: **NGUYEN, Thuy, H.** et al.; Smart & Biggar, 900-55 Metcalfe Street, P.O. Box 2999, Station D, Ottawa, Ontario K1P 5Y6 (CA).

[Continued on next page]

(54) Title: *CHLAMYDIA* ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND USES THEREOF

(57) Abstract: The present invention provides nucleic acids, proteins and vectors for a method of nucleic acid, including DNA, immunization of a host, including humans, against disease caused by infection by a strain of *Chlamydia*, specifically *C. pneumoniae*. The method employs a vector containing a nucleotide sequence encoding a polypeptide of a strain of *Chlamydia pneumoniae* operably linked to a promoter to effect expression of the gene product in the host. The polypeptides are derived from *C. pneumoniae* and are selected from an ATP-binding cassette protein, a secretory locus ORF, an endopeptidase, a protease, a metalloprotease, CLP protease ATPase, a CLP protease subunit, a translycolase / transpeptidase, a CLPc protease and thioredoxin. Modifications are possible within the scope of this invention.

WO 01/85972 A2



**(81) Designated States (national):** AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

**Published:**

— without international search report and to be republished upon receipt of that report

**(84) Designated States (regional):** ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SI, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

**TITLE OF INVENTION**

CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS  
AND USES THEREOF

**REFERENCE TO RELATED APPLICATIONS**

5           This application claims the benefit of U.S.  
Provisional Application Nos. 60/202,672, filed May 8, 2000;  
60/207,852 filed May 30, 2000; 60/211,801, 60/212,044,  
60/211,797, 60/211,796 and 60/211,798 filed June 16, 2000; and  
60/235,335, 60/235,361 and 60/235,398 filed September 26, 2000.

10   **FIELD OF INVENTION**

          The present invention relates to a number of  
*Chlamydia* antigens, including an ATP-binding cassette protein,  
a secretory locus ORF, an endopeptidase, a protease, a  
metalloprotease, CLP protease ATPase, a CLP protease subunit, a  
15   translycolase / transpeptidase, a CLPc protease and  
thioredoxin, and their corresponding DNA molecules, for the  
prevention and treatment of *Chlamydia* infection in mammals.

**BACKGROUND OF THE INVENTION**

*Chlamydiae* are prokaryotes. They exhibit morphologic  
20   and structural similarities to gram-negative bacteria including  
a trilaminar outer membrane, which contains lipopolysaccharide  
and several membrane proteins that are structurally and  
functionally analogous to proteins found in *E coli*. They are  
obligate intra-cellular parasites with a unique biphasic life  
25   cycle consisting of a metabolically inactive but infectious  
extracellular stage and a replicating but non-infectious  
intracellular stage. The replicative stage of the life-cycle  
takes place within a membrane-bound inclusion which sequesters  
the bacteria away from the cytoplasm of the infected host cell.

*C. pneumoniae* is a common human pathogen, originally described as the TWAR strain of *Chlamydia psittaci* but subsequently recognised to be a new species. *C. pneumoniae* is antigenically, genetically and morphologically distinct from  
5 other *Chlamydia* species (*C. trachomatis*, *C. pecorum* and *C. psittaci*). It shows 10% or less DNA sequence homology with either of *C. trachomatis* or *C. psittaci*.

In general, all chlamydiae share a common developmental microbiology and appear to share a common  
10 immunobiology. Genome analysis shown that over 80% of *C. pneumoniae* and *C. trachomatis* protein-coding genes are orthologs that share a similar genome organization.

*C. pneumoniae* is the third most common cause of community acquired pneumonia, only less frequent than  
15 *Streptococcus pneumoniae* and *Mycoplasma pneumoniae* (Grayston et al. (1995) Journal of Infectious Diseases 168:1231; Campos et al. (1995) Investigation of Ophthalmology and Visual Science 36:1477). It can also cause upper respiratory tract symptoms and disease, including bronchitis and sinusitis (Grayston et  
20 al. (1995) Journal of Infectious Diseases 168:1231; Grayston et al (1990) Journal of Infectious Diseases 161:618-625; Marrie (1993) Clinical Infectious Diseases. 18:501-513; Wang et al (1986) Chlamydial infections Cambridge University Press, Cambridge. p. 329. The great majority of the adult population  
25 (over 60%) has antibodies to *C. pneumoniae* (Wang et al (1986) Chlamydial infections. Cambridge University Press, Cambridge. p. 329), indicating past infection which was unrecognized or asymptomatic.

*C. pneumoniae* infection usually presents as an acute  
30 respiratory disease (i.e., cough, sore throat, hoarseness, and fever; abnormal chest sounds on auscultation). For most patients, the cough persists for 2 to 6 weeks, and recovery is



slow. In approximately 10% of these cases, upper respiratory tract infection is followed by bronchitis or pneumonia.

Furthermore, during a *C. pneumoniae* epidemic, subsequent co-infection with pneumococcus has been noted in about half of these pneumonia patients, particularly in the infirm and the elderly. As noted above, there is increasing evidence that *C. pneumoniae* infection is also linked to diseases other than respiratory infections.

The reservoir for the organism is presumably people. In contrast to *C. psittaci* infections, there is no known bird or animal reservoir. Transmission has not been clearly defined. It may result from direct contact with secretions, from fomites, or from airborne spread. There is a long incubation period, which may last for many months. Based on analysis of epidemics, *C. pneumoniae* appears to spread slowly through a population (case-to-case interval averaging 30 days) because infected persons are inefficient transmitters of the organism. Susceptibility to *C. pneumoniae* is universal. Reinfections occur during adulthood, following the primary infection as a child. *C. pneumoniae* appears to be an endemic disease throughout the world, noteworthy for superimposed intervals of increased incidence (epidemics) that persist for 2 to 3 years. *C. trachomatis* infection does not confer cross-immunity to *C. pneumoniae*. Infections are easily treated with oral antibiotics, tetracycline or erythromycin (2 g/d, for at least 10 to 14 d). A recently developed drug, azithromycin, is highly effective as a single-dose therapy against chlamydial infections.

In most instances, *C. pneumoniae* infection is often mild and without complications, and up to 90% of infections are subacute or unrecognized. Among children in industrialized countries, infections have been thought to be rare up to the age of 5 y, although a recent study (E Normann et al, *Chlamydia*

*pneumoniae* in children with acute respiratory tract infections, Acta Paediatrica, 1998, Vol 87, Iss 1, pp 23-27) has reported that many children in this age group show PCR evidence of infection despite being seronegative, and estimates a  
5 prevalence of 17-19% in 2-4 y olds. In developing countries, the seroprevalence of *C. pneumoniae* antibodies among young children is elevated, and there are suspicions that *C. pneumoniae* may be an important cause of acute lower respiratory tract disease and mortality for infants and children in  
10 tropical regions of the world.

From seroprevalence studies and studies of local epidemics, the initial *C. pneumoniae* infection usually happens between the ages of 5 and 20 y. In the USA, for example, there are estimated to be 30,000 cases of childhood pneumonia each  
15 year caused by *C. pneumoniae*. Infections may cluster among groups of children or young adults (e.g., school pupils or military conscripts).

*C. pneumoniae* causes 10 to 25% of community-acquired lower respiratory tract infections (as reported from Sweden,  
20 Italy, Finland, and the USA). During an epidemic, *C. pneumoniae* infection may account for 50 to 60% of the cases of pneumonia. During these periods, also, more episodes of mixed infections with *S. pneumoniae* have been reported.

Reinfection during adulthood is common; the clinical  
25 presentation tends to be milder. Based on population seroprevalence studies, there tends to be increased exposure with age, which is particularly evident among men. Some investigators have speculated that a persistent, asymptomatic *C. pneumoniae* infection state is common.

30 In adults of middle age or older, *C. pneumoniae* infection may progress to chronic bronchitis and sinusitis. A study in the USA revealed that the incidence of pneumonia

caused by *C. pneumoniae* in persons younger than 60 years is 1 case per 1,000 persons per year; but in the elderly, the disease incidence rose three-fold. *C. pneumoniae* infection rarely leads to hospitalization, except in patients with an  
5 underlying illness.

Of considerable importance is the association of atherosclerosis and *C. pneumoniae* infection. There are several epidemiological studies showing a correlation of previous infections with *C. pneumoniae* and heart attacks, coronary  
10 artery and carotid artery disease (Saikku et al. (1988) Lancet;ii:983-986; Thom et al. (1992) JAMA 268:68-72; Linnanmaki et al. (1993), Circulation 87:1030; Saikku et al. (1992) Annals Internal Medicine 116:273-287; Melnick et al (1993) American Journal of Medicine 95:499). Moreover, the organisms  
15 has been detected in atheromas and fatty streaks of the coronary, carotid, peripheral arteries and aorta (Shor et al. (1992) South African. Medical Journal 82:158-161; Kuo et al. (1993) Journal of Infectious Diseases 167:841-849; Kuo et al. (1993) Arteriosclerosis and Thrombosis 13:1501-1504; Campbell  
20 et al (1995) Journal of Infectious Diseases 172:585; Chiu et al. Circulation, 1997. Circulation. 96:2144-2148). Viable *C. pneumoniae* has been recovered from the coronary and carotid artery (Ramirez et al (1996) Annals of Internal Medicine 125:979-982; Jackson et al. 1997. J. Infect. Dis. 176:292-295).  
25 Furthermore, it has been shown that *C. pneumoniae* can induce changes of atherosclerosis in a rabbit model (Fong et al. 1997. Journal of Clinical Microbiology 35:48 and Laitinen et al. 1997. Infect. Immun. 65:4832-4835). Taken together, these results indicate that it is highly probable that *C. pneumoniae*  
30 can cause atherosclerosis in humans, though the epidemiological importance of chlamydial atherosclerosis remains to be demonstrated.

A number of recent studies have also indicated an association between *C. pneumoniae* infection and asthma. Infection has been linked to wheezing, asthmatic bronchitis, adult-onset asthma and acute exacerbations of asthma in adults, and small-scale studies have shown that prolonged antibiotic treatment was effective at greatly reducing the severity of the disease in some individuals (Hahn DL, et al. Evidence for *Chlamydia pneumoniae* infection in steroid-dependent asthma. Ann Allergy Asthma Immunol. 1998 Jan; 80(1): 45-49.; Hahn DL, et al. Association of *Chlamydia pneumoniae* IgA antibodies with recently symptomatic asthma. Epidemiol Infect. 1996 Dec; 117(3): 513-517; Bjornsson E, et al. Serology of *chlamydia* in relation to asthma and bronchial hyperresponsiveness. Scand J Infect Dis. 1996; 28(1): 63-69.; Hahn DL. Treatment of *Chlamydia pneumoniae* infection in adult asthma: a before-after trial. J Fam Pract. 1995 Oct; 41(4): 345-351.; Allegra L, et al. Acute exacerbations of asthma in adults: role of *Chlamydia pneumoniae* infection. Eur Respir J. 1994 Dec; 7(12): 2165-2168.; Hahn DL, et al. Association of *Chlamydia pneumoniae* (strain TWAR) infection with wheezing, asthmatic bronchitis, and adult-onset asthma. JAMA. 1991 Jul 10; 266(2): 225-230).

In light of these results a protective vaccine against *C. pneumoniae* infection would be of considerable importance. There is not yet an effective vaccine for any human chlamydial infection. It is conceivable that an effective vaccine can be developed using physically or chemically inactivated *Chlamydiae*. However, such a vaccine does not have a high margin of safety. In general, safer vaccines are made by genetically manipulating the organism by attenuation or by recombinant means.

A disease associated with *C. trachomatis* infection is trachoma, a sequela of ocular infection. This disease continues to be a major cause of preventable blindness, with an

estimated 500 million cases of active trachoma worldwide (seven million include blindness from conjunctival scarring and eyelid deformities). In the last two decades, genital chlamydial infection has been identified as a major public health problem because of the recognition that chlamydial infection is associated with disease syndromes such as non-gonococcal urethritis, mucopurulent cervicitis, pelvic inflammatory disease (PID), ectopic pregnancy, and tubal infertility. The World Health Organization estimated 89 million new cases of genital chlamydial infections worldwide in 1995. In the United States, each year an estimated four million new cases occur and 50,000 women become infertile as a result of infection.

Studies with *C. trachomatis* and *C. psittaci* indicate that safe and effective vaccine against *Chlamydia* is an attainable goal. For example, mice which have recovered from a lung infection with *C. trachomatis* are protected from infertility induced by a subsequent vaginal challenge (Pal et al. (1996) Infection and Immunity. 64:5341). Similarly, sheep immunized with inactivated *C. psittaci* were protected from subsequent chlamydial-induced abortions and stillbirths (Jones et al. (1995) Vaccine 13:715). In a mouse model, protection from chlamydial infections has been associated with Th1 immune responses, particularly CD8+ CTL response (Rottenberg et al. 1999. J. Immunol. 162:2829-2836 and Penttila et al. 1999. Immunology. 97:490-496) and it is unlikely that similar responses will need to be induced in humans to confer protection. However, antigens able to elicit a protective immune response against *C. pneumoniae* are largely unknown. The presence of sufficiently high titres of neutralising antibody at mucosal surfaces can also exert a protective effect (Cotter et al. (1995) Infection and Immunity 63:4704).

Antigenic variation within the species *C. pneumoniae* is not well documented due to insufficient genetic information,

though variation is expected to exist based on *C. trachomatis*. Serovars of *C. trachomatis* are defined on the basis of antigenic variation in the major outer membrane protein (MOMP), but published *C. pneumoniae* MOMP gene sequences show no  
5 variation between several diverse isolates of the organism (Campbell et al. Infection and Immunity (1990) 58:93; McCafferty et al. Infection and Immunity (1995) 63:2387-9; Gaydos et al. Infection and Immunity. (1992) 60(12):5319-5323). The gene encoding a 76 kDa antigen has been cloned from a  
10 single strain of *C. pneumoniae* and the sequence published (Perez Melgosa et al. Infection and Immunity. (1994) 62:880). An operon encoding the 9 kDa and 60 kDa cyteine-rich outer membrane protein genes has been described (Watson et al., Nucleic Acids Res (1990) 18:5299; Watson et al., Microbiology  
15 (1995) 141:2489). Many antigens recognized by immune sera to *C. pneumoniae* are conserved across all *chlamydiae*, but 98 kDa, 76 kDa and several other proteins may be *C. pneumoniae*-specific (Knudsen et al. Infect. Immun. 1999. 67:375-383; Perez Melgosa et al. Infection and Immunity. 1994. 62:880; Melgosa et al.,  
20 FEMS Microbiol Lett 1993. 112 :199;, Campbell et al., J. Clin. Microbiol. 1990. 28 :1261; Iijima et al., J. Clin. Microbiol. 1994. 32:583). Antisera to 76kDa and 54kDa antigens have been reported to neutralize *C. pneumoniae in vitro* (Perez Melgosa et al. 1994. Infect. Immun. 62:880-886 and Wiedman-Al-Ahmad et al.  
25 1997. Clin. Diagn. Lab. Immunol. 4:700-704). An assessment of the number and relative frequency of any *C. pneumoniae* serotypes, and the defining antigens, is not yet possible. The entire genome sequence of *C. pneumoniae* strain CWL-029 is now known (<http://chlamydia-www.berkeley.edu:4231/>) and as further  
30 sequences become available a better understanding of antigenic variation may be gained.

Many antigens recognised by immune sera to *C. pneumoniae* are conserved across all *chlamydiae*, but 98kDa,

76 kDa and 54 kDa proteins appear to be *C. pneumoniae*-specific (Campos et al. (1995) Investigation of Ophthalmology and Visual Science 36:1477; Marrie (1993) Clinical Infectious Diseases. 18:501-513; Wiedmann-Al-Ahmad M, et al. Reactions of polyclonal  
5 and neutralizing anti-p54 monoclonal antibodies with an isolated, species-specific 54-kilodalton protein of *Chlamydia pneumoniae*. Clin Diagn Lab Immunol. 1997 Nov; 4(6): 700-704).

Immunoblotting of isolates with sera from patients does show variation of blotting patterns between isolates,  
10 indicating that serotypes *C. pneumoniae* may exist (Grayston et al. (1995) Journal of Infectious Diseases 168:1231; Ramirez et al (1996) Annals of Internal Medicine 125:979-982). However, the results are potentially confounded by the infection status of the patients, since immunoblot profiles of a patient's sera  
15 change with time post-infection. An assessment of the number and relative frequency of any serotypes, and the defining antigens, is not yet possible.

The use of DNA immunization to elicit a protective immune response in Balb/c mice against pulmonary infection with  
20 the mouse pneumonitis (MoPn) strain of *Chlamydia trachomatis* has recently been described (Zhang et al. 1997. J. Infect. Dis. 76:1035-1040 and Zhang et al. 1999. Immunology. 96:314-321). Recently the genome sequence from *C. pneumoniae* strain CM1 (ATCC #1360-VR) has been disclosed by Griffais in WO99/27105  
25 on June 3, 1999.

Accordingly, a need exists for identifying and isolating polynucleotide sequences of *C. pneumoniae* for use in preventing and treating *Chlamydia* infection.

**SUMMARY OF THE INVENTION**

The present invention provides purified and isolated polynucleotide molecules that encode a *Chlamydia* polypeptide selected from: an ATP-binding cassette protein, a secretory  
5 locus ORF, an endopeptidase, a protease, a metalloprotease, CLP protease ATPase, a CLP protease subunit, a transglycolase / transpeptidase, a CLPc protease and thioredoxin. The polynucleotide molecules can be used in methods to prevent, treat, and diagnose *Chlamydia* infection. In one embodiment of  
10 the invention, the polynucleotide molecules is DNA that encode a polypeptide of any one of SEQ ID Nos: 2, 4, 6, 8, 10, 12, 14, 16, 18 and 20.

Another form of the invention provides polypeptides corresponding to an isolated DNA molecule. Amino acid  
15 sequences of the corresponding encoded polypeptides are shown in one embodiment as SEQ ID Nos: 2, 4, 6, 8, 10, 12, 14, 16, 18 and 20.

Those skilled in the art will readily understand that the invention, having provided the polynucleotide sequences  
20 encoding *Chlamydia* polypeptides, also provides polynucleotides encoding fragments derived from such polypeptides. Moreover, the invention is understood to provide mutants and derivatives of such polypeptides and fragments derived therefrom, which result from the addition, deletion, or substitution of non-  
25 essential amino acids as described herein. Those skilled in the art would also readily understand that the invention, having provided the polynucleotide sequences encoding *Chlamydia* polypeptides, further provides monospecific antibodies that specifically bind to such polypeptides.

30 The present invention has wide application and includes expression cassettes, vectors, and cells transformed or transfected with the polynucleotides of the invention.



Accordingly, the present invention further provides (i) a method for producing a polypeptide of the invention in a recombinant host system and related expression cassettes, vectors, and transformed or transfected cells; (ii) a vaccine,  
5 or a live vaccine vector such as a pox virus, *Salmonella typhimurium*, or *Vibrio cholerae* vector, containing a polypeptide or a polynucleotide of the invention, such vaccines and vaccine vectors being useful for, e.g., preventing and treating *Chlamydia* infection, in combination with a diluent or  
10 carrier, and related pharmaceutical compositions and associated therapeutic and/or prophylactic methods; (iii) a therapeutic and/or prophylactic use of an RNA or DNA molecule of the invention, either in a naked form or formulated with a delivery vehicle, a polypeptide or combination of polypeptides, or a  
15 monospecific antibody of the invention, and related pharmaceutical compositions; (iv) a method for diagnosing the presence of *Chlamydia* in a biological sample, which can involve the use of a DNA or RNA molecule, a monospecific antibody, or a polypeptide of the invention; and (v) a method for purifying a  
20 polypeptide of the invention by antibody-based affinity chromatography.

One aspect of the invention provides a vaccine comprising a vaccine vector and at least one first nucleic acid selected from any one of:

25 (i) a nucleic acid sequence set forth in any one of SEQ ID Nos: 1, 3, 5, 7, 9, 11, 13, 15, 17 and 19;

(ii) a nucleic acid sequence which encodes a polypeptide encoded by any one of SEQ ID Nos: 1, 3, 5, 7, 9, 11, 13, 15, 17 and 19;

30 (iii) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid

sequence to the polypeptide encoded by any one of SEQ ID Nos:  
1, 3, 5, 7, 9, 11, 13, 15, 17 and 19; and

(iv) a nucleic acid sequence which encodes a  
polypeptide whose sequence is set forth in any one of SEQ ID  
5 Nos: 2, 4, 6, 8, 10, 12, 14, 16, 18 and 20;

(v) a nucleic acid sequence as defined in (i), (ii)  
or (iv), which has been modified to encode a modified  
polypeptide, wherein the modified polypeptide retains  
immunogenicity and is at least 75% identical in amino acid  
10 sequence to the corresponding polypeptide encoded by the  
nucleic acid of (i), (ii) or (iv);

wherein each first nucleic acid is capable of being  
expressed.

Another aspect of the invention provides a vaccine  
15 comprising a vaccine vector and at least one first nucleic acid  
selected from any one of:

(i) a nucleic acid sequence comprising at least 36  
consecutive nucleotides from any one of SEQ ID Nos: 1, 3, 5, 7,  
9, 11, 13, 15, 17 and 19;

20 (ii) a nucleic acid sequence which encodes an  
immunogenic fragment comprising at least 12 consecutive amino  
acids from any one of SEQ ID Nos: 2, 4, 6, 8, 10, 12, 14, 16,  
18 and 20;

(iii) a nucleic acid sequence as defined in (i) or  
25 (ii), which has been modified to encode a modified polypeptide,  
wherein the modified polypeptide retains immunogenicity and is  
at least 75% identical in amino acid sequence to the  
corresponding fragment of (i) or (ii);

wherein each first nucleic acid is capable of being expressed.

#### **BRIEF DESCRIPTION OF THE DRAWINGS**

The present invention will be further understood from  
5 the following description with reference to the drawings, in which:

Figure 1 shows the nucleotide sequence of the gene encoding an ATP-binding cassette (SEQ ID No: 1) and the deduced amino acid sequence of the ATP-binding cassette from *Chlamydia*  
10 *pneumoniae* (SEQ ID No: 2).

Figure 2 shows the nucleotide sequence of the gene encoding a secretory locus ORF (SEQ ID No: 3) and the deduced amino acid sequence of the secretory locus ORF from *Chlamydia pneumoniae* (SEQ ID No: 4).

15 Figure 3 shows the nucleotide sequence of the gene encoding an endopeptidase (SEQ ID No: 5) and the deduced amino acid sequence of the endopeptidase from *Chlamydia pneumoniae* (SEQ ID No: 6).

Figure 4 shows the nucleotide sequence of the gene  
20 encoding a protease (SEQ ID No: 7) and the deduced amino acid sequence of the protease from *Chlamydia pneumoniae* (SEQ ID No: 8).

Figure 5 shows the nucleotide sequence of the gene encoding a metalloprotease (SEQ ID No: 9) and the deduced amino  
25 acid sequence of the metalloprotease from *Chlamydia pneumoniae* (SEQ ID No: 10).

Figure 6 shows the nucleotide sequence of the gene encoding CLP protease ATPase (SEQ ID No: 11) and the deduced

amino acid sequence of the CLP protease ATPase from *Chlamydia pneumoniae* (SEQ ID No: 12).

Figure 7 shows the nucleotide sequence of the gene encoding a CLP protease subunit (SEQ ID No: 13) and the deduced  
5 amino acid sequence of the CLP protease subunit from *Chlamydia pneumoniae* (SEQ ID No: 14).

Figure 8 shows the nucleotide sequence of the gene encoding a transglycolase / transpeptidase (SEQ ID No: 15) and the deduced amino acid sequence of the transglycolase /  
10 transpeptidase from *Chlamydia pneumoniae* (SEQ ID No: 16).

Figure 9 shows the nucleotide sequence of the gene encoding a CLPc protease (SEQ ID No: 17) and the deduced amino acid sequence of the CLPc protease from *Chlamydia pneumoniae* (SEQ ID No: 18).

15 Figure 10 shows the nucleotide sequence of the gene encoding thioredoxin (SEQ ID No: 19) and the deduced amino acid sequence of thioredoxin from *Chlamydia pneumoniae* (SEQ ID No: 20).

Figure 11 shows the restriction enzyme analysis of  
20 the *C. pneumoniae* gene encoding an ATP-binding cassette.

Figure 12 shows shows the restriction enzyme analysis of the *C. pneumoniae* gene encoding a secretory locus ORF.

Figure 13 shows the restriction enzyme analysis of the *C. pneumoniae* gene encoding an endopeptidase.

25 Figure 14 shows the restriction enzyme analysis of the *C. pneumoniae* gene encoding a protease.

Figure 15 shows the restriction enzyme analysis of the *C. pneumoniae* gene encoding a metalloprotease.

Figure 16 shows the restriction enzyme analysis of the *C. pneumoniae* gene encoding CLP protease ATPase.

Figure 17 shows the restriction enzyme analysis of the *C. pneumoniae* gene encoding a CLP protease subunit.

5           Figure 18 shows the restriction enzyme analysis of the *C. pneumoniae* gene encoding a translycolase / transpeptidase.

Figure 19 shows the restriction enzyme analysis of the *C. pneumoniae* gene encoding a CLPc protease.

10           Figure 20 shows the restriction enzyme analysis of the *C. pneumoniae* gene encoding thioredoxin.

Figure 21 shows the construction and elements of plasmid pCACPNM213.

15           Figure 22 shows the construction and elements of plasmid pCACPNM882.

Figure 23 shows the construction and elements of plasmid pCACPNM208.

Figure 24 shows the construction and elements of plasmid pCACPNM1096.

20           Figure 25 shows the construction and elements of plasmid pCACPNM1097.

Figure 26 shows the construction and elements of plasmid pCACPNM908.

25           Figure 27 shows the construction and elements of plasmid pCACPNM909.

Figure 28 shows the construction and elements of plasmid pCACPNM440.

Figure 29 shows the construction and elements of plasmid pCACPNM459.

Figure 30 shows the construction and elements of plasmid pCACPNM708.

5           Figure 31 illustrates protection against *C. pneumoniae* infection by pCACPNM213 following DNA immunization.

Figure 32 illustrates protection against *C. pneumoniae* infection by pCACPNM882 following DNA immunization.

10           Figure 33 illustrates protection against *C. pneumoniae* infection by pCACPNM208 following DNA immunization.

Figure 34 illustrates protection against *C. pneumoniae* infection by pCACPNM1096 following DNA immunization.

Figure 35 illustrates protection against *C. pneumoniae* infection by pCACPNM1097 following DNA immunization.

15           Figure 36 illustrates protection against *C. pneumoniae* infection by pCACPNM908 following DNA immunization.

Figure 37 illustrates protection against *C. pneumoniae* infection by pCACPNM909 following DNA immunization.

20           Figure 38 illustrates protection against *C. pneumoniae* infection by pCACPNM2440 following DNA immunization.

Figure 39 illustrates protection against *C. pneumoniae* infection by pCACPNM459 following DNA immunization.

Figure 40 illustrates protection against *C. pneumoniae* infection by pCACPNM708 following DNA immunization.

**DETAILED DESCRIPTION OF INVENTION**

Open reading frames (ORFs) encoding a number of Chlamydial proteins have been identified from the *C. pneumoniae* genome. These proteins include an ATP-binding cassette protein, a secretory locus ORF, an endopeptidase, a protease, a metalloprotease, CLP protease ATPase, a CLP protease subunit, a translycolase / transpeptidase, a CLPc protease and thioredoxin. The gene encoding each of these polypeptides has been inserted into an expression plasmid and shown to confer immune protection against chlamydial infection. Accordingly, any one of these and related polypeptides can be used to prevent and treat *Chlamydia* infection.

According to a first aspect of the invention, isolated polynucleotides are provided which encode *Chlamydia* polypeptides, whose amino acid sequences are shown in SEQ ID No: 2, 4, 6, 8, 10, 12, 14, 16, 18 and 20.

The term "isolated polynucleotide" is defined as a polynucleotide removed from the environment in which it naturally occurs. For example, a naturally-occurring DNA molecule present in the genome of a living bacteria or as part of a gene bank is not isolated, but the same molecule separated from the remaining part of the bacterial genome, as a result of, e.g., a cloning event (amplification), is isolated. Typically, an isolated DNA molecule is free from DNA regions (e.g., coding regions) with which it is immediately contiguous at the 5' or 3' end, in the naturally occurring genome. Such isolated polynucleotides may be part of a vector or a composition and still be defined as isolated in that such a vector or composition is not part of the natural environment of such polynucleotide.

The polynucleotide of the invention is either RNA or DNA (cDNA, genomic DNA, or synthetic DNA), or modifications,

variants, homologs or fragments thereof. The DNA is either double-stranded or single-stranded, and, if single-stranded, is either the coding strand or the non-coding (anti-sense) strand. Any one of the sequences that encode the polypeptides of the invention as shown in any one of SEQ ID Nos: 2, 4, 6, 8, 10, 12, 14, 16, 18 and 20 is (a) a coding sequence, (b) a ribonucleotide sequence derived from transcription of (a), or (c) a coding sequence which uses the redundancy or degeneracy of the genetic code to encode the same polypeptides. By "polypeptide" or "protein" is meant any chain of amino acids, regardless of length or post-translational modification (e.g., glycosylation or phosphorylation). Both terms are used interchangeably in the present application.

Consistent with the first aspect of the invention, amino acid sequences are provided which are homologous to any one of SEQ ID Nos: 2, 4, 6, 8, 10, 12, 14, 16, 18 and 20. As used herein, "homologous amino acid sequence" is any polypeptide which is encoded, in whole or in part, by a nucleic acid sequence which hybridizes at 25-35°C below critical melting temperature ( $T_m$ ), to any portion of the nucleic acid sequence of any one of SEQ ID Nos: 1, 3, 5, 7, 9, 11, 13, 15, 17 and 19. A homologous amino acid sequence is one that differs from an amino acid sequence shown in any one of SEQ ID Nos: 2, 4, 6, 8, 10, 12, 14, 16, 18 and 20 by one or more conservative amino acid substitutions. Such a sequence also encompasses serotypic variants (defined below) as well as sequences containing deletions or insertions which retain inherent characteristics of the polypeptide such as immunogenicity. Preferably, such a sequence is at least 75%, preferably at least 78%, more preferably at least 80%, even more preferably at least 85%, 88% or 90%, and most preferably at least 93%, 95% or 98% identical to any one of SEQ ID Nos: 2, 4, 6, 8, 10, 12, 14, 16, 18 and 20.



Homologous amino acid sequences include sequences that are identical or substantially identical to any one of SEQ ID Nos: 2, 4, 6, 8, 10, 12, 14, 16, 18 and 20. By "amino acid sequence substantially identical" is meant a sequence that is  
5 at least 90%, preferably 95%, more preferably 97%, and most preferably 99% identical to an amino acid sequence of reference and that preferably differs from the sequence of reference by a majority of conservative amino acid substitutions.

Conservative amino acid substitutions are  
10 substitutions among amino acids of the same class. These classes include, for example, amino acids having uncharged polar side chains, such as asparagine, glutamine, serine, threonine, and tyrosine; amino acids having basic side chains, such as lysine, arginine, and histidine; amino acids having  
15 acidic side chains, such as aspartic acid and glutamic acid; and amino acids having nonpolar side chains, such as glycine, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan, and cysteine.

Homology is measured using sequence analysis software  
20 such as Sequence Analysis Software Package of the Genetics Computer Group, University of Wisconsin Biotechnology Center, 1710 University Avenue, Madison, WI 53705. Amino acid sequences are aligned to maximize identity. Gaps may be artificially introduced into the sequence to attain proper  
25 alignment. Once the optimal alignment has been set up, the degree of homology is established by recording all of the positions in which the amino acids of both sequences are identical, relative to the total number of positions.

Homologous polynucleotide sequences are defined in a  
30 similar way. Preferably, a homologous sequence is one that is at least 45%, more preferably 50%, 55%, 60%, 65%, 70%, 75%, 80%, and even more preferably 85%, 87%, 90%, 93%, 96% and most

preferably 99% identical to the coding sequence of any one of SEQ ID Nos: 1, 3, 5, 7, 9, 11, 13, 15, 17 and 19.

Consistent with the first aspect of the invention, polypeptides having a sequence homologous to any one of SEQ ID  
5 Nos: 2, 4, 6, 8, 10, 12, 14, 16, 18 and 20 include naturally-occurring allelic variants, as well as mutants or any other non-naturally occurring variants that retain the inherent characteristics of the polypeptide of any one of SEQ ID Nos: 2, 4, 6, 8, 10, 12, 14, 16, 18 and 20.

10 As is known in the art, an allelic variant is an alternate form of a polypeptide that is characterized as having a substitution, deletion, or addition of one or more amino acids that does not alter the biological function of the polypeptide. By "biological function" is meant the function of  
15 the polypeptide in the cells in which it naturally occurs, even if the function is not necessary for the growth or survival of the cells. For example, the biological function of a porin is to allow the entry into cells of compounds present in the extracellular medium. Biological function is distinct from  
20 antigenic property. A polypeptide can have more than one biological function.

Allelic variants are very common in nature. For example, a bacterial species such as *C. pneumoniae*, is usually represented by a variety of strains that differ from each other  
25 by minor allelic variations. Indeed, a polypeptide that fulfills the same biological function in different strains can have an amino acid sequence (and polynucleotide sequence) that is not identical in each of the strains. Despite this variation, an immune response directed generally against many  
30 allelic variants has been demonstrated. In studies of the *Chlamydial* MOMP antigen, cross-strain antibody binding plus neutralization of infectivity occurs despite amino acid

sequence variation of MOMP from strain to strain, indicating that the MOMP, when used as an immunogen, is tolerant of amino acid variations.

Polynucleotides encoding homologous polypeptides or  
5 allelic variants are retrieved by polymerase chain reaction (PCR) amplification of genomic bacterial DNA extracted by conventional methods. This involves the use of synthetic oligonucleotide primers matching upstream and downstream of the 5' and 3' ends of the encoding domain. Suitable primers are  
10 designed according to the nucleotide sequence information provided in any one of SEQ ID Nos: 1, 3, 5, 7, 9, 11, 13, 15, 17 and 19. The procedure is as follows: a primer is selected which consists of 10 to 40, preferably 15 to 25 nucleotides. It is advantageous to select primers containing C and G  
15 nucleotides in a proportion sufficient to ensure efficient hybridization; *i.e.*, an amount of C and G nucleotides of at least 40%, preferably 50% of the total nucleotide content. A standard PCR reaction contains typically 0.5 to 5 Units of Taq DNA polymerase per 100  $\mu$ L, 20 to 200  $\mu$ M deoxynucleotide each,  
20 preferably at equivalent concentrations, 0.5 to 2.5 mM magnesium over the total deoxynucleotide concentration,  $10^5$  to  $10^6$  target molecules, and about 20 pmol of each primer. About 25 to 50 PCR cycles are performed, with an annealing temperature 15°C to 5°C below the true  $T_m$  of the primers. A  
25 more stringent annealing temperature improves discrimination against incorrectly annealed primers and reduces incorporation of incorrect nucleotides at the 3' end of primers. A denaturation temperature of 95°C to 97°C is typical, although higher temperatures may be appropriate for dematuration of G+C-  
30 rich targets. The number of cycles performed depends on the starting concentration of target molecules, though typically more than 40 cycles is not recommended as non-specific background products tend to accumulate.

An alternative method for retrieving polynucleotides encoding homologous polypeptides or allelic variants is by hybridization screening of a DNA or RNA library. Hybridization procedures are well-known in the art and are described in Ausubel *et al.*, (Ausubel *et al.*, Current Protocols in Molecular Biology, John Wiley & Sons Inc., 1994), Silhavy *et al.* (Silhavy *et al.* Experiments with Gene Fusions, Cold Spring Harbor Laboratory Press, 1984), and Davis *et al.* (Davis *et al.* A Manual for Genetic Engineering: Advanced Bacterial Genetics, Cold Spring Harbor Laboratory Press, 1980)). Important parameters for optimizing hybridization conditions are reflected in a formula used to obtain the critical melting temperature above which two complementary DNA strands separate from each other (Casey & Davidson, Nucl. Acid Res. (1977) 4:1539). For polynucleotides of about 600 nucleotides or larger, this formula is as follows:  $T_m = 81.5 + 0.41 \times (\% \text{ G+C}) + 16.6 \log (\text{cation ion concentration}) - 0.63 \times (\% \text{ formamide}) - 600/\text{base number}$ . Under appropriate stringency conditions, hybridization temperature ( $T_h$ ) is approximately 20 to 40°C, 20 to 25°C, or, preferably 30 to 40°C below the calculated  $T_m$ . Those skilled in the art will understand that optimal temperature and salt conditions can be readily determined.

For the polynucleotides of the invention, stringent conditions are achieved for both pre-hybridizing and hybridizing incubations (i) within 4-16 hours at 42°C, in 6 x SSC containing 50% formamide, or (ii) within 4-16 hours at 65°C in an aqueous 6 x SSC solution (1 M NaCl, 0.1 M sodium citrate (pH 7.0)). Typically, hybridization experiments are performed at a temperature from 60 to 68°C, e.g. 65°C. At such a temperature, stringent hybridization conditions can be achieved in 6xSSC, preferably in 2xSSC or 1xSSC, more preferably in 0.5xSSC, 0.3xSSC or 0.1xSSC (in the absence of formamide). 1xSSC contains 0.15 M NaCl and 0.015 M sodium citrate.

Useful homologs and fragments thereof that do not occur naturally are designed using known methods for identifying regions of an antigen that are likely to tolerate amino acid sequence changes and/or deletions. As an example, homologous polypeptides from different species are compared; conserved sequences are identified. The more divergent sequences are the most likely to tolerate sequence changes. Homology among sequences may be analyzed using, as an example, the BLAST homology searching algorithm of Altschul *et al.*, Nucleic Acids Res.; 25:3389-3402 (1997). Alternatively, sequences are modified such that they become more reactive to T- and/or B-cells, based on computer-assisted analysis of probable T- or B-cell epitopes. Yet another alternative is to mutate a particular amino acid residue or sequence within the polypeptide *in vitro*, then screen the mutant polypeptides for their ability to prevent or treat *Chlamydia* infection according to the method outlined below.

A person skilled in the art will readily understand that by following the screening process of this invention, it will be determined without undue experimentation whether a particular homolog of any one of SEQ ID Nos: 2, 4, 6, 8, 10, 12, 14, 16, 18 and 20 may be useful in the prevention or treatment of *Chlamydia* infection. The screening procedure comprises the steps:

- (i) immunizing an animal, preferably mouse, with the test homolog or fragment;
- (ii) inoculating the immunized animal with *Chlamydia*;  
and
- (iii) selecting those homologs or fragments which confer protection against *Chlamydia*.

By "conferring protection" is meant that there is a reduction in severity of any of the effects of *Chlamydia* infection, in comparison with a control animal which was not immunized with the test homolog or fragment.

5 Consistent with the first aspect of the invention, polypeptide derivatives are provided that are partial sequences of any one of SEQ ID Nos: 2, 4, 6, 8, 10, 12, 14, 16, 18 and 20, partial sequences of polypeptide sequences homologous to any one of SEQ ID Nos: 2, 4, 6, 8, 10, 12, 14, 16, 18 and 20,  
10 polypeptides derived from full-length polypeptides by internal deletion, and fusion proteins.

It is an accepted practice in the field of immunology to use fragments and variants of protein immunogens as vaccines, as all that is required to induce an immune response  
15 to a protein is a small (e.g., 8 to 10 amino acid) immunogenic region of the protein. Various short synthetic peptides corresponding to surface-exposed antigens of pathogens other than *Chlamydia* have been shown to be effective vaccine antigens against their respective pathogens, e.g. an 11 residue peptide  
20 of murine mammary tumor virus (Casey & Davidson, Nucl. Acid Res. (1977) 4:1539), a 16-residue peptide of Semliki Forest virus (Snijders *et al.*, 1991. J. Gen. Virol. 72:557-565), and two overlapping peptides of 15 residues each from canine parvovirus (Langeveld *et al.*, Vaccine 12(15):1473-1480, 1994)

25 Accordingly, it will be readily apparent to one skilled in the art, having read the present description, that partial sequences of any one of SEQ ID Nos: 2, 4, 6, 8, 10, 12, 14, 16, 18 and 20 or their homologous amino acid sequences are inherent to the full-length sequences and are taught by the  
30 present invention. Such polypeptide fragments preferably are at least 12 amino acids in length. Advantageously, they are at least 15 amino acids, preferably at least 20, 25, 30, 35, 40,

45, 50 amino acids, more preferably at least 55, 60, 65, 70, 75 amino acids, and most preferably at least 80, 85, 90, 95, 100 amino acids in length.

Polynucleotides of 30 to 600 nucleotides encoding  
5 partial sequences of sequences homologous to any one of SEQ ID  
Nos: 2, 4, 6, 8, 10, 12, 14, 16, 18 and 20 are retrieved by PCR  
amplification using the parameters outlined above and using  
primers matching the sequences upstream and downstream of the  
5' and 3' ends of the fragment to be amplified. The template  
10 polynucleotide for such amplification is either the full length  
polynucleotide homologous to any one of SEQ ID Nos: 1, 3, 5, 7,  
9, 11, 13, 15, 17 and 19, or a polynucleotide contained in a  
mixture of polynucleotides such as a DNA or RNA library. As an  
alternative method for retrieving the partial sequences,  
15 screening hybridization is carried out under conditions  
described above and using the formula for calculating  $T_m$ .  
Where fragments of 30 to 600 nucleotides are to be retrieved,  
the calculated  $T_m$  is corrected by subtracting  
(600/polynucleotide size in base pairs) and the stringency  
20 conditions are defined by a hybridization temperature that is  
5 to 10°C below  $T_m$ . Where oligonucleotides shorter than 20-30  
bases are to be obtained, the formula for calculating the  $T_m$  is  
as follows:  $T_m = 4 \times (G+C) + 2 (A+T)$ . For example, an  
18 nucleotide fragment of 50% G+C would have an approximate  $T_m$   
25 of 54°C. Short peptides that are fragments of any one of SEQ  
ID Nos: 2, 4, 6, 8, 10, 12, 14, 16, 18 and 20 or its homologous  
sequences, are obtained directly by chemical synthesis (E.  
Gross and H. J. Meinhofer, 4 The Peptides: Analysis, Synthesis,  
Biology; Modern Techniques of Peptide Synthesis, John Wiley &  
30 Sons (1981), and M. Bodanzki, Principles of Peptide Synthesis,  
Springer -Verlag (1984)).

Useful polypeptide derivatives, e.g., polypeptide  
fragments, are designed using computer-assisted analysis of

amino acid sequences. This would identify probable surface-exposed, antigenic regions (Hughes *et al.*, 1992. *Infect. Immun.* 60(9):3497). Analysis of 6 amino acid sequences contained in any one of SEQ ID Nos: 2, 4, 6, 8, 10, 12, 14, 16, 18 and 20, based on the product of flexibility and hydrophobicity propensities using the program SEQSEE (Wishart DS, *et al.* "SEQSEE: a comprehensive program suite for protein sequence analysis." *Comput Appl Biosci.* 1994 Apr;10(2):121-32), reveal potential B- and T-cell epitopes which may be used as a basis for selecting useful immunogenic fragments and variants. This analysis uses a reasonable combination of external surface features that is likely to be recognized by antibodies. Probable T-cell epitopes for HLA-A0201 MHC subclass may be revealed by an algorithms that emulate an approach developed at the NIH (Parker KC, *et al.* "Peptide binding to MHC class I molecules: implications for antigenic peptide prediction." *Immunol Res* 1995;14(1):34-57). The potential B-cell and T-cell epitopes are shown in Tables 2, 5, 7, 9, 11, 13, 15, 17 and 19 and SEQ ID NOS: 41 to 74. Sequences which are substantially identical to SEQ ID NOS: 41 to 74, or which are conservatively substituted variants of SEQ ID NOS: 41 to 74, are expected to be functional epitopes and are within the scope of the invention.

Epitopes which induce a protective T cell-dependent immune response are present throughout the length of the polypeptide. However, some epitopes may be masked by secondary and tertiary structures of the polypeptide. To reveal such masked epitopes large internal deletions are created which remove much of the original protein structure and exposes the masked epitopes. Such internal deletions sometimes effect the additional advantage of removing immunodominant regions of high variability among strains.



Polynucleotides encoding polypeptide fragments and polypeptides having large internal deletions are constructed using standard methods (Ausubel *et al.*, Current Protocols in Molecular Biology, John Wiley & Sons Inc., 1994). Such methods  
5 include standard PCR, inverse PCR, restriction enzyme treatment of cloned DNA molecules, or the method of Kunkel *et al.* (Kunkel *et al.* Proc. Natl. Acad. Sci. USA (1985) 82:448). Components for these methods and instructions for their use are readily available from various commercial sources such as  
10 Stratagene. Once the deletion mutants have been constructed, they are tested for their ability to prevent or treat *Chlamydia* infection as described above.

As used herein, a fusion polypeptide is one that contains a polypeptide or a polypeptide derivative of the  
15 invention fused at the N- or C-terminal end to any other polypeptide (hereinafter referred to as a peptide tail). A simple way to obtain such a fusion polypeptide is by translation of an in-frame fusion of the polynucleotide sequences, *i.e.*, a hybrid gene. The hybrid gene encoding the  
20 fusion polypeptide is inserted into an expression vector which is used to transform or transfect a host cell. Alternatively, the polynucleotide sequence encoding the polypeptide or polypeptide derivative is inserted into an expression vector in which the polynucleotide encoding the peptide tail is already  
25 present. Such vectors and instructions for their use are commercially available, *e.g.* the pMal-c2 or pMal-p2 system from New England Biolabs, in which the peptide tail is a maltose binding protein, the glutathione-S-transferase system of Pharmacia, or the His-Tag system available from Novagen. These  
30 and other expression systems provide convenient means for further purification of polypeptides and derivatives of the invention.

An advantageous example of a fusion polypeptide is one where the polypeptide or homolog or fragment of the invention is fused to a polypeptide having adjuvant activity, such as subunit B of either cholera toxin or *E. coli* heat-labile toxin. Another advantageous fusion is one where the polypeptide, homolog or fragment is fused to a strong T-cell epitope or B-cell epitope. Such an epitope may be one known in the art (e.g. the Hepatitis B virus core antigen, D.R. Millich *et al.*, "Antibody production to the nucleocapsid and envelope of the Hepatitis B virus primed by a single synthetic T cell site", *Nature*. 1987. 329:547-549), or one which has been identified in another polypeptide of the invention based on computer-assisted analysis of probable T- or B-cell epitopes. Consistent with this aspect of the invention is a fusion polypeptide comprising T- or B-cell epitopes from any one of SEQ ID Nos: 2, 4, 6, 8, 10, 12, 14, 16, 18 and 20 or its homolog or fragment, wherein the epitopes are derived from multiple variants of said polypeptide or homolog or fragment, each variant differing from another in the location and sequence of its epitope within the polypeptide. Such a fusion is effective in the prevention and treatment of *Chlamydia* infection since it optimizes the T- and B-cell response to the overall polypeptide, homolog or fragment.

To effect fusion, the polypeptide of the invention is fused to the N-, or preferably, to the C-terminal end of the polypeptide having adjuvant activity or T- or B-cell epitope. Alternatively, a polypeptide fragment of the invention is inserted internally within the amino acid sequence of the polypeptide having adjuvant activity. The T- or B-cell epitope may also be inserted internally within the amino acid sequence of the polypeptide of the invention.

Consistent with the first aspect, the polynucleotides of the invention also encode hybrid precursor polypeptides

containing heterologous signal peptides, which mature into polypeptides of the invention. By "heterologous signal peptide" is meant a signal peptide that is not found in naturally-occurring precursors of polypeptides of the invention.

Polynucleotide molecules according to the invention, including RNA, DNA, or modifications or combinations thereof, have various applications. A DNA molecule is used, for example, (i) in a process for producing the encoded polypeptide in a recombinant host system, (ii) in the construction of vaccine vectors such as poxviruses, which are further used in methods and compositions for preventing and/or treating *Chlamydia* infection, (iii) as a vaccine agent (as well as an RNA molecule), in a naked form or formulated with a delivery vehicle and, (iv) in the construction of attenuated *Chlamydia* strains that can over-express a polynucleotide of the invention or express it in a non-toxic, mutated form.

Selected genes from pathogenic micro-organisms within an eukaryotic expression plasmid are useful as vaccines. Expression plasmids contain methylated CpG motifs that elicit innate cytokine responses that promote the canalization of CD4 T cell responses to a Th1 cytokine secretion pattern. The intracellular synthesis of the microbial protein, especially within transfected professional antigen-presenting cells, facilitates the presentation of antigen on class I and class II molecules and the induction of cell-mediated immunity. The use of one or a number of microbial protein-coding genes allows the presentation of protective antigens to the immune system to occur in the absence of microbe-directed immune evasion mechanisms and in the absence of competing or pathologic antigens. Immune responses primed by DNA vaccines are also readily amplified by protein-antigen immunization. Thus,

immunization with DNA vaccines is particularly relevant to chlamydial vaccine design.

Accordingly, a second aspect of the invention encompasses (i) an expression cassette containing a DNA molecule of the invention placed under the control of the elements required for expression, in particular under the control of an appropriate promoter; (ii) an expression vector containing an expression cassette of the invention; (iii) a procaryotic or eucaryotic cell transformed or transfected with an expression cassette and/or vector of the invention, as well as (iv) a process for producing a polypeptide or polypeptide derivative encoded by a polynucleotide of the invention, which involves culturing a procaryotic or eucaryotic cell transformed or transfected with an expression cassette and/or vector of the invention, under conditions that allow expression of the DNA molecule of the invention and, recovering the encoded polypeptide or polypeptide derivative from the cell culture.

A recombinant expression system is selected from procaryotic and eucaryotic hosts. Eucaryotic hosts include yeast cells (e.g., *Saccharomyces cerevisiae* or *Pichia pastoris*), mammalian cells (e.g., COS1, NIH3T3, or JEG3 cells), arthropods cells (e.g., *Spodoptera frugiperda* (SF9) cells), and plant cells. A preferred expression system is a procaryotic host such as *E. coli*. Bacterial and eucaryotic cells are available from a number of different sources including commercial sources to those skilled in the art, e.g., the American Type Culture Collection (ATCC; Rockville, Maryland). Commercial sources of cells used for recombinant protein expression also provide instructions for usage of the cells.

The choice of the expression system depends on the features desired for the expressed polypeptide. For example,

it may be useful to produce a polypeptide of the invention in a particular lipidated form or any other form.

One skilled in the art would readily understand that not all vectors and expression control sequences and hosts  
5 would be expected to express equally well the polynucleotides of this invention. With the guidelines described below, however, a selection of vectors, expression control sequences and hosts may be made without undue experimentation and without departing from the scope of this invention.

10 In selecting a vector, the host must be chosen that is compatible with the vector which is to exist and possibly replicate in it. Considerations are made with respect to the vector copy number, the ability to control the copy number, expression of other proteins such as antibiotic resistance. In  
15 selecting an expression control sequence, a number of variables are considered. Among the important variable are the relative strength of the sequence (e.g. the ability to drive expression under various conditions), the ability to control the sequence's function, compatibility between the polynucleotide  
20 to be expressed and the control sequence (e.g. secondary structures are considered to avoid hairpin structures which prevent efficient transcription). In selecting the host, unicellular hosts are selected which are compatible with the selected vector, tolerant of any possible toxic effects of the  
25 expressed product, able to secrete the expressed product efficiently if such is desired, to be able to express the product in the desired conformation, to be easily scaled up, and to which ease of purification of the final product.

The choice of the expression cassette depends on the  
30 host system selected as well as the features desired for the expressed polypeptide. Typically, an expression cassette includes a promoter that is functional in the selected host

system and can be constitutive or inducible; a ribosome binding site; a start codon (ATG) if necessary; a region encoding a signal peptide, e.g., a lipitation signal peptide; a DNA molecule of the invention; a stop codon; and optionally a 3' terminal region (translation and/or transcription terminator). The signal peptide encoding region is adjacent to the polynucleotide of the invention and placed in proper reading frame. The signal peptide-encoding region is homologous or heterologous to the DNA molecule encoding the mature polypeptide and is compatible with the secretion apparatus of the host used for expression. The open reading frame constituted by the DNA molecule of the invention, solely or together with the signal peptide, is placed under the control of the promoter so that transcription and translation occur in the host system. Promoters and signal peptide encoding regions are widely known and available to those skilled in the art and include, for example, the promoter of *Salmonella typhimurium* (and derivatives) that is inducible by arabinose (promoter araB) and is functional in Gram-negative bacteria such as *E. coli* (as described in U.S. Patent No. 5,028,530 and in Cagnon et al., (Cagnon et al., Protein Engineering (1991) 4(7):843)); the promoter of the gene of bacteriophage T7 encoding RNA polymerase, that is functional in a number of *E. coli* strains expressing T7 polymerase (described in U.S. Patent No. 4,952,496); OspA lipitation signal peptide ; and RlpB lipitation signal peptide (Takase et al., J. Bact. (1987) 169:5692).

The expression cassette is typically part of an expression vector, which is selected for its ability to replicate in the chosen expression system. Expression vectors (e.g., plasmids or viral vectors) can be chosen, for example, from those described in Pouwels et al. (Cloning Vectors: A

Laboratory Manual 1985, Supp. 1987). Suitable expression vectors can be purchased from various commercial sources.

Methods for transforming/transfecting host cells with expression vectors are well-known in the art and depend on the host system selected as described in Ausubel *et al.*, (Ausubel *et al.*, Current Protocols in Molecular Biology, John Wiley & Sons Inc., 1994).

Upon expression, a recombinant polypeptide of the invention (or a polypeptide derivative) is produced and remains in the intracellular compartment, is secreted/excreted in the extracellular medium or in the periplasmic space, or is embedded in the cellular membrane. The polypeptide is recovered in a substantially purified form from the cell extract or from the supernatant after centrifugation of the recombinant cell culture. Typically, the recombinant polypeptide is purified by antibody-based affinity purification or by other well-known methods that can be readily adapted by a person skilled in the art, such as fusion of the polynucleotide encoding the polypeptide or its derivative to a small affinity binding domain. Antibodies useful for purifying by immunoaffinity the polypeptides of the invention are obtained as described below.

A polynucleotide of the invention can also be useful as a vaccine. There are two major routes, either using a viral or bacterial host as gene delivery vehicle (live vaccine vector) or administering the gene in a free form, *e.g.*, inserted into a plasmid. Therapeutic or prophylactic efficacy of a polynucleotide of the invention is evaluated as described below.

Accordingly, a third aspect of the invention provides (i) a vaccine vector such as a poxvirus, containing a DNA molecule of the invention, placed under the control of elements

required for expression; (ii) a composition of matter comprising a vaccine vector of the invention, together with a diluent or carrier; specifically (iii) a pharmaceutical composition containing a therapeutically or prophylactically effective amount of a vaccine vector of the invention; (iv) a method for inducing an immune response against *Chlamydia* in a mammal (e.g., a human; alternatively, the method can be used in veterinary applications for treating or preventing *Chlamydia* infection of animals, e.g., cats or birds), which involves administering to the mammal an immunogenically effective amount of a vaccine vector of the invention to elicit a protective or therapeutic immune response to *Chlamydia* ; and particularly, (v) a method for preventing and/or treating a *Chlamydia* (e.g., *C. trachomatis*, *C. psittaci*, *C. pneumonia*, *C. pecorum*) infection, which involves administering a prophylactic or therapeutic amount of a vaccine vector of the invention to an infected individual. Additionally, the third aspect of the invention encompasses the use of a vaccine vector of the invention in the preparation of a medicament for preventing and/or treating *Chlamydia* infection.

As used herein, a vaccine vector expresses one or several polypeptides or derivatives of the invention. The vaccine vector may express additionally a cytokine, such as interleukin-2 (IL-2) or interleukin-12 (IL-12), that enhances the immune response (adjuvant effect). It is understood that each of the components to be expressed is placed under the control of elements required for expression in a mammalian cell.

Consistent with the third aspect of the invention is a composition comprising several vaccine vectors, each of them capable of expressing a polypeptide or derivative of the invention. A composition may also comprise a vaccine vector capable of expressing an additional *Chlamydia* antigen, or a



subunit, fragment, homolog, mutant, or derivative thereof;  
optionally together with or a cytokine such as IL-2 or IL-12.

. A general principle is that recognition of a  
particular antigen is not in itself sufficient to produce an  
5 effective immune response. In some cases, a cell-mediated  
response is appropriate; in others, antibody.

Antigens of microorganisms vary considerably in their  
accessibility to cells of the immune system. Antigens which  
normally occur inside a pathogen may become accessible only  
10 when the pathogen or an infected cell is killed. Even antigens  
expressed at the cell surface may present only a limited range  
of their potential epitopes for antibody binding, depending on  
their orientation in the membrane. Protective structures, such  
as bacterial capsules, further limit the effective recognition  
15 of epitopes.

A distinction should be drawn between the overall  
composition of the immune response, those components of it  
which are important in the resolution of infection and the  
components which are responsible for the prevention of re-  
20 infection. In many cases, particular elements of the immune  
response are critically important; for example, cell-mediated  
immunity in leprosy. Even when considering a particular  
effector system, the response directed against some antigens is  
often much more effective than the responses to others. Immune  
25 responses to particular microbial antigens have different  
degrees of relevance to anti-microbial immunity, depending on  
the nature of the organism, its pathogenicity and the nature of  
the immune response it initiates.

The primary effectors against extracellular pathogens  
30 are antibody and complement. Binding of antibody to receptors  
on the pathogen can prevent it from attaching to its target  
cell. Antibody alone, or more effectively in association with

complement, opsonizes pathogens for uptake by phagocytes expressing Fc receptors and complement receptors CR1 and CR3. Usually this will lead to intracellular destruction of the pathogen but if the phagocyte is unable to destroy it and is a facultative host cell, then antibody may actually promote the spread of infection. Such an eventuality, however, depends on the dynamic balance between the actions of the humoral and cell-mediated immune responses.

Sometimes effective antibodies must be of the right class to activate appropriate effectors. The important antigens are those involved in evasion of immune effector mechanisms; that is, pili, fimbriae and capsular antigens which constitute the major antigens of the outer layer of bacteria. Often epitope specificity is important, since it determines whether complement is deposited in a position to damage the outer membrane. There are also numerous protein antigens which can induce an antibody response; however, although the antibody response is partly species-specific and may be diagnostically useful, it is largely irrelevant to immunity. This is most obvious in lepromatous leprosy, where the patients have weak cell-mediated immunity, high levels of specific antibody and tissues heavily infected with bacteria.

In some cases, a particular type of antibody response is mandatory for clearance of the pathogen. This is true of many bacterial infections, where specific antibodies to surface antigens are necessary to neutralize the bacterial defences and opsonize the bacteria for phagocytes.

There are also cases where responses to individual antigens are essential for host immunity. The simplest examples are the toxins produced by the causative agents of diphtheria, tetanus and clostridial enteritis. The damage produced directly by the infectious agent in these diseases is

slight by comparison with that produced by the secreted toxins. Consequently, protection against these conditions involves immunization to toxoids. Nevertheless, the immune system must still eradicate the primary site of the bacterial infection if  
5 the disease is to be resolved. The target antigens for bactericidal antibodies are extremely diverse and include LPS, capsular polysaccharides and other outer membrane proteins. Virulence factors can also provide good immunogens in a vaccine.

10               Tables 1, 3, 4, 6, 8, 10, 12, 14, 16 and 18, as well as corresponding Figures 31 to 40, demonstrate that the polypeptides disclosed herein are immunogenic. Furthermore, these Figures demonstrate that the polypeptides disclosed herein confer immunoprotection from *Chlamydia* infection, as  
15 evidenced by accelerated clearance of pulmonary infection. Such reduction in the severity of effects of *Chlamydia* infection is evidence that the polypeptides have generated an active functional immune response against the pathogen, rather than a mere antibody response against the antigen.

20               Animal models have been used to define the immunobiologic feature of *C. trachomatis* infection. The mouse model is particularly informative, largely because of the ready availability of immune reagents for murine studies and the development of transgenic and knockout (KO) mice. *C.*  
25 *trachomatis* mouse pneumonitis (MoPn) is the most widely tested biovar among the three *C. trachomatis* biovars (trachoma, lymphogranuloma venereum, and MoPn). Although human biovars have also been used in animal models, they normally require high inocula or pretreatment with progesterone. MoPn, which  
30 was originally isolated from mouse tissues, is thought to be a natural murine pathogen and thus offers an evolutionarily adapted pathogen for analysis of host-pathogen interactions.

The significant progress in chlamydial immunobiology based on murine models of MoPn infection has extended and clarified recent immunoepidemiologic studies in humans (Yang and Brunham (1998) Can J Infect Dis; 9:99-108). In particular, since the discovery of T helper (Th) 1 and 2 subsets, cytokine patterns have been shown to be critical in the regulation of immune responses to a variety of infectious agents including chlamydiae. Clinical investigation has shown that trachoma patients with severe conjunctival scarring have impaired cell-mediated immune responses to *C. trachomatis* and high IgG antibody titers (Yang and Brunham (1999) Curr Opin Infect Dis; 12:47-52). Cytokine analysis shows increased interleukin (IL)-4 and reduced interferon (IFN)- $\gamma$  production in subjects with scarring disease due to *C. trachomatis* infection compared with controls without scarring disease.

Vaccination methods for treating or preventing infection in a mammal comprises use of a vaccine vector of the invention to be administered by any conventional route, particularly to a mucosal (e.g., ocular, intranasal, oral, gastric, pulmonary, intestinal, rectal, vaginal, or urinary tract) surface or via the parenteral (e.g., subcutaneous, intradermal, intramuscular, intravenous, or intraperitoneal) route. Preferred routes depend upon the choice of the vaccine vector. Treatment may be effected in a single dose or repeated at intervals. The appropriate dosage depends on various parameters understood by skilled artisans such as the vaccine vector itself, the route of administration or the condition of the mammal to be vaccinated (weight, age and the like).

Live vaccine vectors available in the art include viral vectors such as adenoviruses and poxviruses as well as bacterial vectors, e.g., *Shigella*, *Salmonella*, *Vibrio cholerae*, *Lactobacillus*, Bacille bilié de Calmette-Guérin (BCG), and *Streptococcus*.

An example of an adenovirus vector, as well as a method for constructing an adenovirus vector capable of expressing a DNA molecule of the invention, are described in U.S. Patent No. 4,920,209. Poxvirus vectors include vaccinia and canary pox virus, described in U.S. Patent No. 4,722,848 and U.S. Patent No. 5,364,773, respectively. (Also see, e.g., Tartaglia et al., Virology (1992) 188:217) for a description of a vaccinia virus vector and Taylor et al, Vaccine (1995) 13:539 for a reference of a canary pox.) Poxvirus vectors capable of expressing a polynucleotide of the invention are obtained by homologous recombination as described in Kieny et al., Nature (1984) 312:163 so that the polynucleotide of the invention is inserted in the viral genome under appropriate conditions for expression in mammalian cells. Generally, the dose of vaccine viral vector, for therapeutic or prophylactic use, can be of from about  $1 \times 10^4$  to about  $1 \times 10^{11}$ , advantageously from about  $1 \times 10^7$  to about  $1 \times 10^{10}$ , preferably of from about  $1 \times 10^7$  to about  $1 \times 10^9$  plaque-forming units per kilogram. Preferably, viral vectors are administered parenterally; for example, in 3 doses, 4 weeks apart. It is preferable to avoid adding a chemical adjuvant to a composition containing a viral vector of the invention and thereby minimizing the immune response to the viral vector itself.

Non-toxicogenic *Vibrio cholerae* mutant strains that are useful as a live oral vaccine are known. Mekalanos et al., Nature (1983) 306:551 and U.S. Patent No. 4,882,278 describe strains which have a substantial amount of the coding sequence of each of the two *ctxA* alleles deleted so that no functional *cholerae* toxin is produced. WO 92/11354 describes a strain in which the *irgA* locus is inactivated by mutation; this mutation can be combined in a single strain with *ctxA* mutations. WO 94/01533 describes a deletion mutant lacking functional *ctxA* and *attRS1* DNA sequences. These mutant strains are genetically

engineered to express heterologous antigens, as described in WO 94/19482. An effective vaccine dose of a *Vibrio cholerae* strain capable of expressing a polypeptide or polypeptide derivative encoded by a DNA molecule of the invention contains  
5 about  $1 \times 10^5$  to about  $1 \times 10^9$ , preferably about  $1 \times 10^6$  to about  $1 \times 10^8$ , viable bacteria in a volume appropriate for the selected route of administration. Preferred routes of administration include all mucosal routes; most preferably, these vectors are administered intranasally or orally.

10           Attenuated *Salmonella typhimurium* strains, genetically engineered for recombinant expression of heterologous antigens or not, and their use as oral vaccines are described in Nakayama et al. (Bio/Technology (1988) 6:693) and WO 92/11361. Preferred routes of administration include  
15 all mucosal routes; most preferably, these vectors are administered intranasally or orally.

Other bacterial strains used as vaccine vectors in the context of the present invention are described for *Shigella flexneri* in High et al., EMBO (1992) 11:1991 and Sizemore et  
20 al., Science (1995) 270:299; for *Streptococcus gordonii* in Medaglini et al., Proc. Natl. Acad. Sci. USA (1995) 92:6868; and for Bacille Calmette Guerin in Flynn J.L., Cell. Mol. Biol. (1994) 40 (suppl. I):31, WO 88/06626, WO 90/00594, WO 91/13157, WO 92/01796, and WO 92/21376.

25           In bacterial vectors, the polynucleotide of the invention is inserted into the bacterial genome or remains in a free state as part of a plasmid.

The composition comprising a vaccine bacterial vector of the present invention may further contain an adjuvant. A  
30 number of adjuvants are known to those skilled in the art. Preferred adjuvants are selected as provided below.

Accordingly, a fourth aspect of the invention provides (i) a composition of matter comprising a polynucleotide of the invention, together with a diluent or carrier; (ii) a pharmaceutical composition comprising a therapeutically or prophylactically effective amount of a polynucleotide of the invention; (iii) a method for inducing an immune response against *Chlamydia* in a mammal by administration of an immunogenically effective amount of a polynucleotide of the invention to elicit a protective immune response to *Chlamydia*; and particularly, (iv) a method for preventing and/or treating a *Chlamydia* (e.g., *C. trachomatis*, *C. psittaci*, *C. pneumoniae*, or *C. pecorum*) infection, by administering a prophylactic or therapeutic amount of a polynucleotide of the invention to an infected individual. Additionally, the fourth aspect of the invention encompasses the use of a polynucleotide of the invention in the preparation of a medicament for preventing and/or treating *Chlamydia* infection. A preferred use includes the use of a DNA molecule placed under conditions for expression in a mammalian cell, especially in a plasmid that is unable to replicate in mammalian cells and to substantially integrate in a mammalian genome.

Use of the polynucleotides of the invention include their administration to a mammal as a vaccine, for therapeutic or prophylactic purposes. Such polynucleotides are used in the form of DNA as part of a plasmid that is unable to replicate in a mammalian cell and unable to integrate into the mammalian genome. Typically, such a DNA molecule is placed under the control of a promoter suitable for expression in a mammalian cell. The promoter functions either ubiquitously or tissue-specifically. Examples of non-tissue specific promoters include the early Cytomegalovirus (CMV) promoter (described in U.S. Patent No. 4,168,062) and the Rous Sarcoma Virus promoter (described in Norton & Coffin, *Molec. Cell Biol.* (1985) 5:281).

An example of a tissue-specific promoter is the desmin promoter which drives expression in muscle cells (Li et al., Gene (1989) 78:243, Li & Paulin, J. Biol. Chem. (1991) 266:6562 and Li & Paulin, J. Biol. Chem. (1993) 268:10403). Use of promoters is well-known to those skilled in the art. Useful vectors are described in numerous publications, specifically WO 94/21797 and Hartikka et al., Human Gene Therapy (1996) 7:1205.

Polynucleotides of the invention which are used as vaccines encode either a precursor or a mature form of the corresponding polypeptide. In the precursor form, the signal peptide is either homologous or heterologous. In the latter case, a eucaryotic leader sequence such as the leader sequence of the tissue-type plasminogen factor (tPA) is preferred.

As used herein, a composition of the invention contains one or several polynucleotides with optionally at least one additional polynucleotide encoding another *Chlamydia* antigen such as urease subunit A, B, or both, or a fragment, derivative, mutant, or analog thereof. The composition may also contain an additional polynucleotide encoding a cytokine, such as interleukin-2 (IL-2) or interleukin-12 (IL-12) so that the immune response is enhanced. These additional polynucleotides are placed under appropriate control for expression. Advantageously, DNA molecules of the invention and/or additional DNA molecules to be included in the same composition, are present in the same plasmid.

Standard techniques of molecular biology for preparing and purifying polynucleotides are used in the preparation of polynucleotide therapeutics of the invention. For use as a vaccine, a polynucleotide of the invention is formulated according to various methods outlined below.

One method utilizes the polynucleotide in a naked form, free of any delivery vehicles. Such a polynucleotide is



simply diluted in a physiologically acceptable solution such as sterile saline or sterile buffered saline, with or without a carrier. When present, the carrier preferably is isotonic, hypotonic, or weakly hypertonic, and has a relatively low ionic strength, such as provided by a sucrose solution, e.g., a solution containing 20% sucrose.

An alternative method utilizes the polynucleotide in association with agents that assist in cellular uptake. Examples of such agents are (i) chemicals that modify cellular permeability, such as bupivacaine (see, e.g., WO 94/16737), (ii) liposomes for encapsulation of the polynucleotide, or (iii) cationic lipids or silica, gold, or tungsten microparticles which associate themselves with the polynucleotides.

Anionic and neutral liposomes are well-known in the art (see, e.g., Liposomes: A Practical Approach, RPC New Ed, IRL press (1990), for a detailed description of methods for making liposomes) and are useful for delivering a large range of products, including polynucleotides.

Cationic lipids are also known in the art and are commonly used for gene delivery. Such lipids include Lipofectin<sup>TM</sup> also known as DOTMA (N-[1-(2,3-dioleyloxy)propyl]-N,N,N-trimethylammonium chloride), DOTAP (1,2-bis(oleyloxy)-3-(trimethylammonio)propane), DDAB (dimethyldioctadecylammonium bromide), DOGS (dioctadecylamidoglycyl spermine) and cholesterol derivatives such as DC-Chol (3 beta-(N-(N',N'-dimethyl aminomethane)-carbamoyl) cholesterol). A description of these cationic lipids can be found in EP 187,702, WO 90/11092, U.S. Patent No. 5,283,185, WO 91/15501, WO 95/26356, and U.S. Patent No. 5,527,928. Cationic lipids for gene delivery are preferably used in association with a

neutral lipid such as DOPE (dioleoyl phosphatidylethanolamine), as described in WO 90/11092 as an example.

Formulation containing cationic liposomes may optionally contain other transfection-facilitating compounds. A number of them are described in WO 93/18759, WO 93/19768, WO 94/25608, and WO 95/02397. They include spermine derivatives useful for facilitating the transport of DNA through the nuclear membrane (see, for example, WO 93/18759) and membrane-permeabilizing compounds such as GALA, Gramicidine S, and cationic bile salts (see, for example, WO 93/19768).

Gold or tungsten microparticles are used for gene delivery, as described in WO 91/00359, WO 93/17706, and Tang *et al.* Nature (1992) 356:152. The microparticle-coated polynucleotide is injected *via* intradermal or intraepidermal routes using a needleless injection device ("gene gun"), such as those described in U.S. Patent No. 4,945,050, U.S. Patent No. 5,015,580, and WO 94/24263.

The amount of DNA to be used in a vaccine recipient depends, *e.g.*, on the strength of the promoter used in the DNA construct, the immunogenicity of the expressed gene product, the condition of the mammal intended for administration (*e.g.*, the weight, age, and general health of the mammal), the mode of administration, and the type of formulation. In general, a therapeutically or prophylactically effective dose from about 1  $\mu$ g to about 1 mg, preferably, from about 10  $\mu$ g to about 800  $\mu$ g and, more preferably, from about 25  $\mu$ g to about 250  $\mu$ g, can be administered to human adults. The administration can be achieved in a single dose or repeated at intervals.

The route of administration is any conventional route used in the vaccine field. As general guidance, a polynucleotide of the invention is administered *via* a mucosal surface, *e.g.*, an ocular, intranasal, pulmonary, oral,

intestinal, rectal, vaginal, and urinary tract surface; or via a parenteral route, e.g., by an intravenous, subcutaneous, intraperitoneal, intradermal, intraepidermal, or intramuscular route. The choice of administration route depends on the  
5 formulation that is selected. A polynucleotide formulated in association with bupivacaine is advantageously administered into muscles. When a neutral or anionic liposome or a cationic lipid, such as DOTMA or DC-Chol, is used, the formulation can be advantageously injected via intravenous, intranasal  
10 (aerosolization), intramuscular, intradermal, and subcutaneous routes. A polynucleotide in a naked form can advantageously be administered via the intramuscular, intradermal, or subcutaneous routes.

Although not absolutely required, such a composition  
15 can also contain an adjuvant. If so, a systemic adjuvant that does not require concomitant administration in order to exhibit an adjuvant effect is preferable such as, e.g., QS21, which is described in U.S. Patent No. 5,057,546.

The sequence information provided in the present  
20 application enables the design of specific nucleotide probes and primers that are used for diagnostic purposes. Accordingly, a fifth aspect of the invention provides a nucleotide probe or primer having a sequence found in or derived by degeneracy of the genetic code from a sequence shown  
25 in any one of SEQ ID Nos: 1, 3, 5, 7, 9, 11, 13, 15, 17 and 19.

The term "probe" as used in the present application refers to DNA (preferably single stranded) or RNA molecules (or modifications or combinations thereof) that hybridize under the stringent conditions, as defined above, to nucleic acid  
30 molecules having any one of SEQ ID Nos: 1, 3, 5, 7, 9, 11, 13, 15, 17 and 19 or to a sequence homologous to any one of SEQ ID Nos: 1, 3, 5, 7, 9, 11, 13, 15, 17 and 19, or to its

complementary or anti-sense sequence. Generally, probes are significantly shorter than full-length sequences. Such probes contain from about 5 to about 100, preferably from about 10 to about 80, nucleotides. In particular, probes have sequences  
5 that are at least 75%, preferably at least 80% or 85%, more preferably 90% or 95% homologous to a portion of any one of SEQ ID Nos: 1, 3, 5, 7, 9, 11, 13, 15, 17 and 19 or that are complementary to such sequences. Probes may contain modified bases such as inosine, methyl-5-deoxycytidine, deoxyuridine,  
10 dimethylamino-5-deoxyuridine, or diamino-2, 6-purine. Sugar or phosphate residues may also be modified or substituted. For example, a deoxyribose residue may be replaced by a polyamide (Nielsen et al., Science (1991) 254:1497) and phosphate residues may be replaced by ester groups such as diphosphate,  
15 alkyl, arylphosphonate and phosphorothioate esters. In addition, the 2'-hydroxyl group on ribonucleotides may be modified by including such groups as alkyl groups.

Probes of the invention are used in diagnostic tests, as capture or detection probes. Such capture probes are  
20 conventionally immobilized on a solid support, directly or indirectly, by covalent means or by passive adsorption. A detection probe is labelled by a detection marker selected from: radioactive isotopes, enzymes such as peroxidase, alkaline phosphatase, and enzymes able to hydrolyze a  
25 chromogenic, fluorogenic, or luminescent substrate, compounds that are chromogenic, fluorogenic, or luminescent, nucleotide base analogs, and biotin.

Probes of the invention are used in any conventional hybridization technique, such as dot blot (Maniatis et al.,  
30 Molecular Cloning: A Laboratory Manual (1982) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York), Southern blot (Southern, J. Mol. Biol. (1975) 98:503), northern blot (identical to Southern blot with the exception that RNA is

used as a target), or the sandwich technique (Dunn et al., Cell (1977) 12:23). The latter technique involves the use of a specific capture probe and/or a specific detection probe with nucleotide sequences that at least partially differ from each other.

A primer is a probe of usually about 10 to about 40 nucleotides that is used to initiate enzymatic polymerization of DNA in an amplification process (e.g., PCR), in an elongation process, or in a reverse transcription method. Primers used in diagnostic methods involving PCR are labeled by methods known in the art.

As described herein, the invention also encompasses (i) a reagent comprising a probe of the invention for detecting and/or identifying the presence of *Chlamydia* in a biological material; (ii) a method for detecting and/or identifying the presence of *Chlamydia* in a biological material, in which (a) a sample is recovered or derived from the biological material, (b) DNA or RNA is extracted from the material and denatured, and (c) exposed to a probe of the invention, for example, a capture, detection probe or both, under stringent hybridization conditions, such that hybridization is detected; and (iii) a method for detecting and/or identifying the presence of *Chlamydia* in a biological material, in which (a) a sample is recovered or derived from the biological material, (b) DNA is extracted therefrom, (c) the extracted DNA is primed with at least one, and preferably two, primers of the invention and amplified by polymerase chain reaction, and (d) the amplified DNA fragment is produced.

It is apparent that disclosure of a polynucleotide sequence of any one of SEQ ID Nos: 1, 3, 5, 7, 9, 11, 13, 15, 17 and 19, its homologs and partial sequences enable their corresponding amino acid sequences. Accordingly, a sixth

aspect of the invention features a substantially purified polypeptide or polypeptide derivative having an amino acid sequence encoded by a polynucleotide of the invention.

A "substantially purified polypeptide" as used herein  
5 is defined as a polypeptide that is separated from the environment in which it naturally occurs and/or that is free of the majority of the polypeptides that are present in the environment in which it was synthesized. For example, a substantially purified polypeptide is free from cytoplasmic  
10 polypeptides. Those skilled in the art would readily understand that the polypeptides of the invention may be purified from a natural source, *i.e.*, a *Chlamydia* strain, or produced by recombinant means.

Consistent with the sixth aspect of the invention are  
15 polypeptides, homologs or fragments which are modified or treated to enhance their immunogenicity in the target animal, in whom the polypeptide, homolog or fragments are intended to confer protection against *Chlamydia*. Such modifications or treatments include: amino acid substitutions with an amino acid  
20 derivative such as 3-methylhistidine, 4-hydroxyproline, 5-hydroxylysine etc., modifications or deletions which are carried out after preparation of the polypeptide, homolog or fragment, such as the modification of free amino, carboxyl or hydroxyl side groups of the amino acids.

25 Identification of homologous polypeptides or polypeptide derivatives encoded by polynucleotides of the invention which have specific antigenicity is achieved by screening for cross-reactivity with an antiserum raised against the polypeptide of reference having an amino acid sequence of  
30 any one of SEQ ID Nos: 2, 4, 6, 8, 10, 12, 14, 16, 18 and 20. The procedure is as follows: a monospecific hyperimmune antiserum is raised against a purified reference polypeptide, a

fusion polypeptide (for example, an expression product of MBP, GST, or His-tag systems, the description and instructions for use of which are contained in Invitrogen product manuals for pcDNA3.1/Myc-His(+) A, B, and C and for the Xpress™ System  
5 Protein Purification), or a synthetic peptide predicted to be antigenic. Where an antiserum is raised against a fusion polypeptide, two different fusion systems are employed. Specific antigenicity can be determined according to a number of methods, including Western blot (Towbin et al., Proc. Natl.  
10 Acad. Sci. USA (1979) 76:4350), dot blot, and ELISA, as described below.

In a Western blot assay, the product to be screened, either as a purified preparation or a total *E. coli* extract, is submitted to SDS-Page electrophoresis as described by Laemmli  
15 (Nature (1970) 227:680). After transfer to a nitrocellulose membrane, the material is further incubated with the monospecific hyperimmune antiserum diluted in the range of dilutions from about 1:5 to about 1:5000, preferably from about 1:100 to about 1:500. Specific antigenicity is shown once a  
20 band corresponding to the product exhibits reactivity at any of the dilutions in the above range.

In an ELISA assay, the product to be screened is preferably used as the coating antigen. A purified preparation is preferred, although a whole cell extract can also be used.  
25 Briefly, about 100 µl of a preparation at about 10 µg protein/ml are distributed into wells of a 96-well polycarbonate ELISA plate. The plate is incubated for 2 hours at 37°C then overnight at 4°C. The plate is washed with phosphate buffer saline (PBS) containing 0.05% Tween 20  
30 (PBS/Tween buffer). The wells are saturated with 250 µl PBS containing 1% bovine serum albumin (BSA) to prevent non-specific antibody binding. After 1 hour incubation at 37°C, the plate is washed with PBS/Tween buffer. The antiserum is

serially diluted in PBS/Tween buffer containing 0.5% BSA. 100  $\mu$ l of dilutions are added per well. The plate is incubated for 90 minutes at 37°C, washed and evaluated according to standard procedures. For example, a goat anti-rabbit peroxidase  
5 conjugate is added to the wells when specific antibodies were raised in rabbits. Incubation is carried out for 90 minutes at 37°C and the plate is washed. The reaction is developed with the appropriate substrate and the reaction is measured by colorimetry (absorbance measured spectrophotometrically).  
10 Under the above experimental conditions, a positive reaction is shown by O.D. values greater than a non immune control serum.

In a dot blot assay, a purified product is preferred, although a whole cell extract can also be used. Briefly, a solution of the product at about 100  $\mu$ g/ml is serially two-fold  
15 diluted in 50 mM Tris-HCl (pH 7.5). 100  $\mu$ l of each dilution are applied to a nitrocellulose membrane 0.45  $\mu$ m set in a 96-well dot blot apparatus (Biorad). The buffer is removed by applying vacuum to the system. Wells are washed by addition of 50 mM Tris-HCl (pH 7.5) and the membrane is air-dried. The  
20 membrane is saturated in blocking buffer (50 mM Tris-HCl (pH 7.5) 0.15 M NaCl, 10 g/L skim milk) and incubated with an antiserum dilution from about 1:50 to about 1:5000, preferably about 1:500. The reaction is revealed according to standard procedures. For example, a goat anti-rabbit peroxidase  
25 conjugate is added to the wells when rabbit antibodies are used. Incubation is carried out 90 minutes at 37°C and the blot is washed. The reaction is developed with the appropriate substrate and stopped. The reaction is measured visually by the appearance of a colored spot, e.g., by colorimetry. Under  
30 the above experimental conditions, a positive reaction is shown once a colored spot is associated with a dilution of at least about 1:5, preferably of at least about 1:500.



Therapeutic or prophylactic efficacy of a polypeptide or derivative of the invention can be evaluated as described below. A seventh aspect of the invention provides (i) a composition of matter comprising a polypeptide of the invention  
5 together with a diluent or carrier; specifically (ii) a pharmaceutical composition containing a therapeutically or prophylactically effective amount of a polypeptide of the invention; (iii) a method for inducing an immune response against *Chlamydia* in a mammal, by administering to the mammal  
10 an immunogenically effective amount of a polypeptide of the invention to elicit a protective immune response to *Chlamydia*; and particularly, (iv) a method for preventing and/or treating a *Chlamydia* (e.g., *C. trachomatis*, *C. psittaci*, *C. pneumoniae*, or *C. pecorum*) infection, by administering a prophylactic or  
15 therapeutic amount of a polypeptide of the invention to an infected individual. Additionally, the seventh aspect of the invention encompasses the use of a polypeptide of the invention in the preparation of a medicament for preventing and/or treating *Chlamydia* infection.

20 As used herein, the immunogenic compositions of the invention are administered by conventional routes known the vaccine field, in particular to a mucosal (e.g., ocular, intranasal, pulmonary, oral, gastric, intestinal, rectal, vaginal, or urinary tract) surface or via the parenteral (e.g.,  
25 subcutaneous, intradermal, intramuscular, intravenous, or intraperitoneal) route. The choice of administration route depends upon a number of parameters, such as the adjuvant associated with the polypeptide. If a mucosal adjuvant is used, the intranasal or oral route is preferred. If a lipid  
30 formulation or an aluminum compound is used, the parenteral route is preferred with the sub-cutaneous or intramuscular route being most preferred. The choice also depends upon the nature of the vaccine agent. For example, a polypeptide of the

invention fused to CTB or LTB is best administered to a mucosal surface.

As used herein, the composition of the invention contains one or several polypeptides or derivatives of the invention. The composition optionally contains at least one additional *Chlamydia* antigen, or a subunit, fragment, homolog, mutant, or derivative thereof.

For use in a composition of the invention, a polypeptide or derivative thereof is formulated into or with liposomes, preferably neutral or anionic liposomes, microspheres, ISCOMS, or virus-like-particles (VLPs) to facilitate delivery and/or enhance the immune response. These compounds are readily available to one skilled in the art; for example, see Liposomes: A Practical Approach, RCP New Ed, IRL press (1990).

Adjuvants other than liposomes and the like are also used and are known in the art. Adjuvants may protect the antigen from rapid dispersal by sequestering it in a local deposit, or they may contain substances that stimulate the host to secrete factors that are chemotactic for macrophages and other components of the immune system. An appropriate selection can conventionally be made by those skilled in the art, for example, from those described below (under the eleventh aspect of the invention).

Treatment is achieved in a single dose or repeated as necessary at intervals, as can be determined readily by one skilled in the art. For example, a priming dose is followed by three booster doses at weekly or monthly intervals. An appropriate dose depends on various parameters including the recipient (e.g., adult or infant), the particular vaccine antigen, the route and frequency of administration, the presence/absence or type of adjuvant, and the desired effect

(e.g., protection and/or treatment), as can be determined by one skilled in the art. In general, a vaccine antigen of the invention is administered by a mucosal route in an amount from about 10 µg to about 500 mg, preferably from about 1 mg to  
5 about 200 mg. For the parenteral route of administration, the dose usually does not exceed about 1 mg, preferably about 100 µg.

When used as vaccine agents, polynucleotides and polypeptides of the invention may be used sequentially as part  
10 of a multistep immunization process. For example, a mammal is initially primed with a vaccine vector of the invention such as a pox virus, e.g., via the parenteral route, and then boosted twice with the polypeptide encoded by the vaccine vector, e.g., via the mucosal route. In another example, liposomes  
15 associated with a polypeptide or derivative of the invention is also used for priming, with boosting being carried out mucosally using a soluble polypeptide or derivative of the invention in combination with a mucosal adjuvant (e.g., LT).

A polypeptide derivative of the invention is also  
20 used in accordance with the seventh aspect as a diagnostic reagent for detecting the presence of anti-*Chlamydia* antibodies, e.g., in a blood sample. Such polypeptides are about 5 to about 80, preferably about 10 to about 50 amino acids in length. They are either labeled or unlabeled,  
25 depending upon the diagnostic method. Diagnostic methods involving such a reagent are described below.

Upon expression of a DNA molecule of the invention, a polypeptide or polypeptide derivative is produced and purified using known laboratory techniques. As described above, the  
30 polypeptide or polypeptide derivative may be produced as a fusion protein containing a fused tail that facilitates purification. The fusion product is used to immunize a small

mammal, e.g., a mouse or a rabbit, in order to raise antibodies against the polypeptide or polypeptide derivative (monospecific antibodies). Accordingly, an eighth aspect of the invention provides a monospecific antibody that binds to a polypeptide or  
5 polypeptide derivative of the invention.

By "monospecific antibody" is meant an antibody that is capable of reacting with a unique naturally-occurring *Chlamydia* polypeptide. An antibody of the invention is either polyclonal or monoclonal. Monospecific antibodies may be  
10 recombinant, e.g., chimeric (e.g., constituted by a variable region of murine origin associated with a human constant region), humanized (a human immunoglobulin constant backbone together with hypervariable region of animal, e.g., murine, origin), and/or single chain. Both polyclonal and monospecific  
15 antibodies may also be in the form of immunoglobulin fragments, e.g., F(ab)'<sub>2</sub> or Fab fragments. The antibodies of the invention are of any isotype, e.g., IgG or IgA, and polyclonal antibodies are of a single isotype or a mixture of isotypes.

Antibodies against the polypeptides, homologs or  
20 fragments of the present invention are generated by immunization of a mammal with a composition comprising said polypeptide, homolog or fragment. Such antibodies may be polyclonal or monoclonal. Methods to produce polyclonal or monoclonal antibodies are well known in the art. For a review,  
25 see "Antibodies, A Laboratory Manual, Cold Spring Harbor Laboratory, Eds. E. Harlow and D. Lane (1988), and D.E. Yelton et al., 1981. Ann. Rev. Biochem. 50:657-680. For monoclonal antibodies, see Kohler & Milstein (1975) Nature 256:495-497.

The antibodies of the invention, which are raised to  
30 a polypeptide or polypeptide derivative of the invention, are produced and identified using standard immunological assays, e.g., Western blot analysis, dot blot assay, or ELISA (see,

e.g., Coligan et al., Current Protocols in Immunology (1994) John Wiley & Sons, Inc., New York, NY). The antibodies are used in diagnostic methods to detect the presence of a *Chlamydia* antigen in a sample, such as a biological sample.

5 The antibodies are also used in affinity chromatography for purifying a polypeptide or polypeptide derivative of the invention. As is discussed further below, such antibodies may be used in prophylactic and therapeutic passive immunization methods.

10               Accordingly, a ninth aspect of the invention provides (i) a reagent for detecting the presence of *Chlamydia* in a biological sample that contains an antibody, polypeptide, or polypeptide derivative of the invention; and (ii) a diagnostic method for detecting the presence of *Chlamydia* in a biological  
15 sample, by contacting the biological sample with an antibody, a polypeptide, or a polypeptide derivative of the invention, such that an immune complex is formed, and by detecting such complex to indicate the presence of *Chlamydia* in the sample or the organism from which the sample is derived.

20               Those skilled in the art will readily understand that the immune complex is formed between a component of the sample and the antibody, polypeptide, or polypeptide derivative, whichever is used, and that any unbound material is removed prior to detecting the complex. It is understood that a  
25 polypeptide reagent is useful for detecting the presence of anti-*Chlamydia* antibodies in a sample, e.g., a blood sample, while an antibody of the invention is used for screening a sample, such as a gastric extract or biopsy, for the presence of *Chlamydia* polypeptides.

30               For diagnostic applications, the reagent (i.e., the antibody, polypeptide, or polypeptide derivative of the invention) is either in a free state or immobilized on a solid

support, such as a tube, a bead, or any other conventional support used in the field. Immobilization is achieved using direct or indirect means. Direct means include passive adsorption (non-covalent binding) or covalent binding between  
5 the support and the reagent. By "indirect means" is meant that an anti-reagent compound that interacts with a reagent is first attached to the solid support. For example, if a polypeptide reagent is used, an antibody that binds to it can serve as an anti-reagent, provided that it binds to an epitope that is not  
10 involved in the recognition of antibodies in biological samples. Indirect means may also employ a ligand-receptor system, for example, where a molecule such as a vitamin is grafted onto the polypeptide reagent and the corresponding receptor immobilized on the solid phase. This is illustrated  
15 by the biotin-streptavidin system. Alternatively, a peptide tail is added chemically or by genetic engineering to the reagent and the grafted or fused product immobilized by passive adsorption or covalent linkage of the peptide tail.

Such diagnostic agents may be included in a kit which  
20 also comprises instructions for use. The reagent is labeled with a detection means which allows for the detection of the reagent when it is bound to its target. The detection means may be a fluorescent agent such as fluorescein isocyanate or fluorescein isothiocyanate, or an enzyme such as horse radish  
25 peroxidase or luciferase or alkaline phosphatase, or a radioactive element such as  $^{125}\text{I}$  or  $^{51}\text{Cr}$ .

Accordingly, a tenth aspect of the invention provides a process for purifying, from a biological sample, a polypeptide or polypeptide derivative of the invention, which  
30 involves carrying out antibody-based affinity chromatography with the biological sample, wherein the antibody is a monospecific antibody of the invention.

For use in a purification process of the invention, the antibody is either polyclonal or monospecific, and preferably is of the IgG type. Purified IgGs is prepared from an antiserum using standard methods (see, e.g., Coligan et al.,  
5 Current Protocols in Immunology (1994) John Wiley & Sons, Inc., New York, NY.). Conventional chromatography supports, as well as standard methods for grafting antibodies, are described in, e.g., Antibodies: A Laboratory Manual, D. Lane, E. Harlow, Eds. (1988) and outlined below.

10 Briefly, a biological sample, such as an *C. pneumoniae* extract preferably in a buffer solution, is applied to a chromatography material, preferably equilibrated with the buffer used to dilute the biological sample so that the polypeptide or polypeptide derivative of the invention (i.e.,  
15 the antigen) is allowed to adsorb onto the material. The chromatography material, such as a gel or a resin coupled to an antibody of the invention, is in either a batch form or a column. The unbound components are washed off and the antigen is then eluted with an appropriate elution buffer, such as a  
20 glycine buffer or a buffer containing a chaotropic agent, e.g., guanidine HCl, or high salt concentration (e.g., 3 M MgCl<sub>2</sub>). Eluted fractions are recovered and the presence of the antigen is detected, e.g., by measuring the absorbance at 280 nm.

An eleventh aspect of the invention provides (i) a  
25 composition of matter comprising a monospecific antibody of the invention, together with a diluent or carrier; (ii) a pharmaceutical composition comprising a therapeutically or prophylactically effective amount of a monospecific antibody of the invention, and (iii) a method for treating or preventing a  
30 *Chlamydia* (e.g., *C. trachomatis*, *C. psittaci*, *C. pneumoniae* or *C. pecorum*) infection, by administering a therapeutic or prophylactic amount of a monospecific antibody of the invention to an infected individual. Additionally, the eleventh aspect

of the invention encompasses the use of a monospecific antibody of the invention in the preparation of a medicament for treating or preventing *Chlamydia* infection.

The monospecific antibody is either polyclonal or  
5 monoclonal, preferably of the IgA isotype (predominantly). In passive immunization, the antibody is administered to a mucosal surface of a mammal, e.g., the gastric mucosa, e.g., orally or intragastrically, advantageously, in the presence of a bicarbonate buffer. Alternatively, systemic administration,  
10 not requiring a bicarbonate buffer, is carried out. A monospecific antibody of the invention is administered as a single active component or as a mixture with at least one monospecific antibody specific for a different *Chlamydia* polypeptide. The amount of antibody and the particular regimen  
15 used are readily determined by one skilled in the art. For example, daily administration of about 100 to 1,000 mg of antibodies over one week, or three doses per day of about 100 to 1,000 mg of antibodies over two or three days, are effective regimens for most purposes.

20 Therapeutic or prophylactic efficacy are evaluated using standard methods in the art, e.g., by measuring induction of a mucosal immune response or induction of protective and/or therapeutic immunity, using, e.g., the *C. pneumoniae* mouse model. Those skilled in the art will readily recognize that  
25 the *C. pneumoniae* strain of the model may be replaced with another *Chlamydia* strain. For example, the efficacy of DNA molecules and polypeptides from *C. pneumoniae* is preferably evaluated in a mouse model using *C. pneumoniae* strain. Protection is determined by comparing the degree of *Chlamydia*  
30 infection to that of a control group. Protection is shown when infection is reduced by comparison to the control group. Such an evaluation is made for polynucleotides, vaccine vectors,



polypeptides and derivatives thereof, as well as antibodies of the invention.

Adjuvants useful in any of the vaccine compositions described above are as follows.

5           Adjuvants for parenteral administration include aluminum compounds, such as aluminum hydroxide, aluminum phosphate, and aluminum hydroxy phosphate. The antigen is precipitated with, or adsorbed onto, the aluminum compound according to standard protocols. Other adjuvants, such as RIBI  
10 (ImmunoChem, Hamilton, MT), are used in parenteral administration.

          Adjuvants for mucosal administration include bacterial toxins, e.g., the cholera toxin (CT), the *E. coli* heat-labile toxin (LT), the *Clostridium difficile* toxin A and  
15 the pertussis toxin (PT), or combinations, subunits, toxoids, or mutants thereof such as a purified preparation of native cholera toxin subunit B (CTB). Fragments, homologs, derivatives, and fusions to any of these toxins are also suitable, provided that they retain adjuvant activity.  
20 Preferably, a mutant having reduced toxicity is used. Suitable mutants are described, e.g., in WO 95/17211 (Arg-7-Lys CT mutant), WO 96/06627 (Arg-192-Gly LT mutant), and WO 95/34323 (Arg-9-Lys and Glu-129-Gly PT mutant). Additional LT mutants that are used in the methods and compositions of the invention  
25 include, e.g., Ser-63-Lys, Ala-69Gly, Glu-110-Asp, and Glu-112-Asp mutants. Other adjuvants, such as a bacterial monophosphoryl lipid A (MPLA) of, e.g., *E. coli*, *Salmonella minnesota*, *Salmonella typhimurium*, or *Shigella flexneri*; saponins, or polylactide glycolide (PLGA) microspheres, is also  
30 be used in mucosal administration.

          Adjuvants useful for both mucosal and parenteral administrations include polyphosphazene (WO 95/02415), DC-chol

(3 b-(N-(N',N'-dimethyl aminomethane)-carbamoyl) cholesterol;  
U.S. Patent No. 5,283,185 and WO 96/14831) and QS-21  
(WO 88/09336).

Any pharmaceutical composition of the invention  
5 containing a polynucleotide, a polypeptide, a polypeptide  
derivative, or an antibody of the invention, is manufactured in  
a conventional manner. In particular, it is formulated with a  
pharmaceutically acceptable diluent or carrier, e.g., water or  
a saline solution such as phosphate buffer saline. In general,  
10 a diluent or carrier is selected on the basis of the mode and  
route of administration, and standard pharmaceutical practice.  
Suitable pharmaceutical carriers or diluents, as well as  
pharmaceutical necessities for their use in pharmaceutical  
formulations, are described in *Remington's Pharmaceutical*  
15 *Sciences*, a standard reference text in this field and in the  
USP/NF.

The invention also includes methods in which  
*Chlamydia* infection are treated by oral administration of a  
*Chlamydia* polypeptide of the invention and a mucosal adjuvant,  
20 in combination with an antibiotic, an antacid, sucralfate, or a  
combination thereof. Examples of such compounds that can be  
administered with the vaccine antigen and the adjuvant are  
antibiotics, including, e.g., macrolides, tetracyclines, and  
derivatives thereof (specific examples of antibiotics that can  
25 be used include azithromycin or doxycyclin or immunomodulators  
such as cytokines or steroids). In addition, compounds  
containing more than one of the above-listed components coupled  
together, are used. The invention also includes compositions  
for carrying out these methods, i.e., compositions containing a  
30 *Chlamydia* antigen (or antigens) of the invention, an adjuvant,  
and one or more of the above-listed compounds, in a  
pharmaceutically acceptable carrier or diluent.

It has recently been shown that the 60kDa cysteine rich membrane protein contains a sequence cross-reactive with the murine alpha-myosin heavy chain epitope M7A-alpha, an epitope conserved in humans (Bachmaier *et al.*, Science (1999) 283:1335). This cross-reactivity is proposed to contribute to the development of cardiovascular disease, so it may be beneficial to remove this epitope, and any other epitopes cross-reactive with human antigens, from the protein if it is to be used as a vaccine. Accordingly, a further embodiment of the present invention includes the modification of the coding sequence, for example, by deletion or substitution of the nucleotides encoding the epitope from polynucleotides encoding the protein, as to improve the efficacy and safety of the protein as a vaccine. A similar approach may be appropriate for any protective antigen found to have unwanted homologies or cross-reactivities with human antigens.

Amounts of the above-listed compounds used in the methods and compositions of the invention are readily determined by one skilled in the art. Treatment/immunization schedules are also known and readily designed by one skilled in the art. For example, the non-vaccine components can be administered on days 1-14, and the vaccine antigen + adjuvant can be administered on days 7, 14, 21, and 28.

#### **EXAMPLES**

The above disclosure generally describes the present invention. A more complete understanding can be obtained by reference to the following specific examples. These examples are described solely for purposes of illustration and are not intended to limit the scope of the invention. Changes in form and substitution of equivalents are contemplated as circumstances may suggest or render expedient. Although specific terms have been employed herein, such terms are

intended in a descriptive sense and not for purposes of limitation.

### Example 1:

These examples illustrate the preparation of plasmid  
5 vectors used in immunoprotection studies.

#### A. Preparation of plasmid vector pCACPNM213

The ATP-binding cassette gene was amplified from  
*Chlamydia pneumoniae* genomic DNA strain CWLO29 by polymerase  
chain reaction (PCR) using a 5' primer  
10 (5' ATAAGAATGCGGCCGCCACCATGAAGATGCATAGGCTTAAACC 3'; SEQ ID  
No:21) and a 3' primer  
(5' GCGCCGGATCCC**ACTTAAGATATCGATATTTT**GAG 3'; SEQ ID No:22).  
The 5' primer contains a NotI restriction site, a ribosome  
binding site, an initiation codon and a sequence at the 5' end  
15 of the ATP-binding cassette protein coding sequence. The 3'  
primer includes the sequence encoding the C-terminal sequence  
of the ATP-binding cassette protein gene and a BamHI  
restriction site. The stop codon was excluded and an additional  
nucleotide was inserted to obtain an in-frame fusion with the  
20 Histidine tag.

After amplification, the PCR fragment was purified  
using QIAquick™ PCR purification kit (Qiagen), digested with  
NotI and BamHI and cloned into the pCA-Myc-His eukaryotic  
expression vector described in Example 2 (Figure 21) with  
25 transcription under control of the human CMV promoter.

#### B. Preparation of plasmid vector pCACPNM882

The secretory locus ORF gene was amplified from  
*Chlamydia pneumoniae* genomic DNA strain CWLO29 by polymerase  
chain reaction (PCR) using a 5' primer  
30 (5' ATAAGAATGCGGCCGCCACCATGCGGTTGGGAAATAAGCCTATGC 3'; SEQ ID

No:23) and a 3' primer

(5' GCGCCGGTACCG**TAATTTAATACTCTTTGAAGGGC** 3'; SEQ ID No:24). The 5' primer contains a NotI restriction site, a ribosome binding site, an initiation codon and a sequence at the 5' end of the secretory locus ORF coding sequence. The 3' primer includes the sequence encoding the C-terminal sequence of the secretory locus ORF protein and a KpnI restriction site. The stop codon was excluded and an additional nucleotide was inserted to obtain an in-frame fusion with the Histidine tag.

After amplification, the PCR fragment was purified using QIAquick™ PCR purification kit (Qiagen), digested with NotI and KpnI and cloned into the pCA-Myc-His eukaryotic expression vector described in Example 2 (Figure 22) with transcription under control of the human CMV promoter.

#### C. Preparation of plasmid vector pCACPNM208

The endopeptidase gene was amplified from *Chlamydia pneumoniae* genomic DNA strain CWLO29 by polymerase chain reaction (PCR) using a 5' primer

(5' ATAAGAATGCGGCCGCCACCATGCTCACCCCTAGGCTTGGAAAGTTCTTG 3'; SEQ

ID No:25) and a 3' primer

(5' GCTTTGGAGGATCCC**CGGAGAGGCTAAGGAGAATGG** 3'; SEQ ID No:26).

The 5' primer contains a NotI restriction site, a ribosome binding site, an initiation codon and a sequence at the 5' end of the endopeptidase protein coding sequence. The 3' primer includes the sequence encoding the C-terminal sequence of the endopeptidase protein gene and a BamHI restriction site. The stop codon was excluded and an additional nucleotide was inserted to obtain an in-frame fusion with the Histidine tag.

After amplification, the PCR fragment was purified using QIAquick™ PCR purification kit (Qiagen), digested with NotI and BamHI and cloned into the pCA-Myc-His eukaryotic

expression vector described in Example 2 (Figure 23) with transcription under control of the human CMV promoter.

D. Preparation of plasmid vector pCACPNM1096

The protease gene was amplified from *Chlamydia pneumoniae* genomic DNA strain CWLO29 by polymerase chain reaction (PCR) using a 5' primer (5' ATAAGAATGCGGCCGCCACCATGAAAAAAGGGAAATTAGGAGCC 3'; SEQ ID No:27) and a 3' primer (5' GCGCCGGATCCC**CGAAGCAGAAGTCGTTGTGGG** 3'; SEQ ID No:28). The 5' primer contains a NotI restriction site, a ribosome binding site, an initiation codon and a sequence at the 5' end of the protease protein coding sequence. The 3' primer includes the sequence encoding the C-terminal sequence of the protease protein gene and a BamHI restriction site. The stop codon was excluded and an additional nucleotide was inserted to obtain an in-frame fusion with the Histidine tag.

After amplification, the PCR fragment was purified using QIAquick™ PCR purification kit (Qiagen), digested with NotI and BamHI and cloned into the pCA-Myc-His eukaryotic expression vector described in Example 2 (Figure 24) with transcription under control of the human CMV promoter.

E. Preparation of plasmid vector pCACPNM1097

The metalloprotease gene was amplified from *Chlamydia pneumoniae* genomic DNA strain CWLO29 by polymerase chain reaction (PCR) using a 5' primer (5' ATAAGAATGCGGCCGCCACCATGAGAAACTTATTTTATGCAATCCTA 3'; SEQ ID No:29) and a 3' primer (5' GCGCCGGATCCC**AGAACAACGGAGTTCCTTTTGG** 3'; SEQ ID No:30). The 5' primer contains a NotI restriction site, a ribosome binding site, an initiation codon and a sequence at the 5' end of the metalloprotease protein coding sequence. The 3' primer

includes the sequence encoding the C-terminal sequence of the metalloprotease protein gene and a BamHI restriction site. The stop codon was excluded and an additional nucleotide was inserted to obtain an in-frame fusion with the Histidine tag.

5           After amplification, the PCR fragment was purified using QIAquick™ PCR purification kit (Qiagen), digested with NotI and BamHI and cloned into the pCA-Myc-His eukaryotic expression vector described in Example 2 (Figure 25) with transcription under control of the human CMV promoter.

10   F. Preparation of plasmid vector pCACP908

          The CLP protease ATPase gene was amplified from *Chlamydia pneumoniae* genomic DNA strain CWL029 by polymerase chain reaction (PCR) using a 5' primer (5' ATAAGAATGCGGCCGCCACCATGAATAAAAAAATCTAACTATTTG 3'; SEQ ID No:31) and a 3' primer (5' GCGCCGGATCCCAGCGATAGCTTCTGGGGTCC 3'; SEQ ID No:32). The 5' primer contains a NotI restriction site, a ribosome binding site, an initiation codon and a sequence at the 5' end of the CLP protease ATPase protein coding sequence. The 3' primer includes the sequence encoding the C-terminal  
15           sequence of the CLP protease ATPase gene and a BamHI  
20           restriction site. The stop codon was excluded and an additional nucleotide was inserted to obtain an in-frame fusion with the Histidine tag.

          After amplification, the PCR fragment was purified  
25           using QIAquick™ PCR purification kit (Qiagen), digested with NotI and BamHI and cloned into the pCA-Myc-His eukaryotic expression vector described in Example 2 (Figure 26) with transcription under control of the human CMV promoter.

G. Preparation of plasmid vector pCACPNM909

The gene encoding CLP protease subunit was amplified from *Chlamydia pneumoniae* genomic DNA strain CWLO29 by polymerase chain reaction (PCR) using a 5' primer

5 (5' ATAAGAATGCGGCCGCCACCATGACACTGGTACCCTATGTTG 3'; SEQ ID No:33) and a 3' primer

(5' GCGCCGGATCCCAGTGCTACTTGTATCCTTATTAG 3'; SEQ ID No:34). The 5' primer contains a NotI restriction site, a ribosome binding site, an initiation codon and a sequence at the 5' end of the CLP protease subunit coding sequence. The 3' primer includes the sequence encoding the C-terminal sequence of the CLP protease subunit gene and a BamHI restriction site. The stop codon was excluded and an additional nucleotide was inserted to obtain an in-frame fusion with the Histidine tag.

15 After amplification, the PCR fragment was purified using QIAquick™ PCR purification kit (Qiagen), digested with NotI and BamHI and cloned into the pCA-Myc-His eukaryotic expression vector described in Example 2 (Figure 27) with transcription under control of the human CMV promoter.

20 H. Preparation of plasmid vector pCACPNM440

The translycolase / transpeptidase gene was amplified from *Chlamydia pneumoniae* genomic DNA strain CWLO29 by polymerase chain reaction (PCR) using a 5' primer

(5' ATAAGAATGCGGCCGCCACCATGAGCTACCGTAAACGTTGACTC 3'; SEQ ID No:35) and a 3' primer

(5' GCGCCGGATCCCCCTCGTTCCCCCTTGTTCGGAG 3'; SEQ ID No:36). The 5' primer contains a NotI restriction site, a ribosome binding site, an initiation codon and a sequence at the 5' end of the translycolase / transpeptidase coding sequence. The 3' primer includes the sequence encoding the C-terminal sequence of the translycolase / transpeptidase gene and a BamHI restriction



site. The stop codon was excluded and an additional nucleotide was inserted to obtain an in-frame fusion with the Histidine tag.

After amplification, the PCR fragment was purified using QIAquick™ PCR purification kit (Qiagen), digested with NotI and BamHI and cloned into the pCA-Myc-His eukaryotic expression vector described in Example 2 (Figure 28) with transcription under control of the human CMV promoter.

#### I. Preparation of plasmid vector pCACPNM459

The gene encoding CLPc protease was amplified from *Chlamydia pneumoniae* genomic DNA strain CWL029 by polymerase chain reaction (PCR) using a 5' primer (5' ATAAGAATGCGGCCGCCACCATGTTTGAGAAGTTCACCTAATAGAGC 3'; SEQ ID No:37) and a 3' primer (5' GCGCCGGTACCGTGATTCCAAGTGAGGGCTAGGG 3'; SEQ ID No:38). The 5' primer contains a NotI restriction site, a ribosome binding site, an initiation codon and a sequence at the 5' end of the CLPc protease coding sequence. The 3' primer includes the sequence encoding the C-terminal sequence of the CLPc protease gene and a KpnI restriction site. The stop codon was excluded and an additional nucleotide was inserted to obtain an in-frame fusion with the Histidine tag.

After amplification, the PCR fragment was purified using QIAquick™ PCR purification kit (Qiagen), digested with NotI and KpnI and cloned into the pCA-Myc-His eukaryotic expression vector described in Example 2 (Figure 29) with transcription under control of the human CMV promoter.

#### J. Preparation of plasmid vector pCACPNM708

The thioredoxin gene was amplified from *Chlamydia pneumoniae* genomic DNA strain CWL029 by polymerase chain

reaction (PCR) using a 5' primer  
(5' ATAAGAATGCGGCCGCCACCATGGTAAAGATCATATCAAGTG 3'; SEQ ID  
No:39) and a 3' primer (5' GCGCCGGATCCCAGCGTGCTTATTGATAAG 3';  
SEQ ID No:40). The 5' primer contains a NotI restriction site,  
5 a ribosome binding site, an initiation codon and a sequence at  
the 5' end of the thioredoxin coding sequence. The 3' primer  
includes the sequence encoding the C-terminal sequence of the  
thioredoxin gene and a BamHI restriction site. The stop codon  
was excluded and an additional nucleotide was inserted to  
10 obtain an in-frame fusion with the Histidine tag.

After amplification, the PCR fragment was purified  
using QIAquick™ PCR purification kit (Qiagen), digested with  
NotI and BamHI and cloned into the pCA-Myc-His eukaryotic  
expression vector described in Example 2 (Figure 30) with  
15 transcription under control of the human CMV promoter.

#### Example 2:

Plasmid pcDNA3.1(-)Myc-His C (Invitrogen) was  
restricted with SpeI and BamHI to remove the CMV promoter and  
the remaining vector fragment was isolated. The CMV promoter  
20 and intron A from plasmid VR-1012 (Vical) was isolated on a  
SpeI / BamHI fragment. The fragments were ligated together to  
produce plasmid pCA/Myc-His.

The NotI/BamHI restricted PCR fragment containing the  
ATP-binding cassette gene was ligated into the NotI and BamHI  
25 restricted plasmid pCA/Myc-His to produce plasmid pCACPNM213  
(Figure 21).

The NotI/KpnI restricted PCR fragment containing the  
Secretory locus ORF gene was ligated into the NotI and KpnI  
restricted plasmid pCA/Myc-His to produce plasmid pCACPNM882  
30 (Figure 22).

The NotI/BamHI restricted PCR fragment containing the endopeptidase gene was ligated into the NotI and BamHI restricted plasmid pCA/Myc-His to produce plasmid pCACPNM208 (Figure 23).

5           The NotI/BamHI restricted PCR fragment containing the Protease gene was ligated into the NotI and BamHI restricted plasmid pCA/Myc-His to produce plasmid pCACPNM1096 (Figure 24).

          The NotI/BamHI restricted PCR fragment containing the Metalloprotease gene was ligated into the NotI and BamHI  
10 restricted plasmid pCA/Myc-His to produce plasmid pCACPNM1097 (Figure 25).

          The NotI/BamHI restricted PCR fragment containing the CLP protease ATPase gene was ligated into the NotI and BamHI restricted plasmid pCA/Myc-His to produce plasmid pCACPNM908  
15 (Figure 26).

          The NotI/BamHI restricted PCR fragment containing the CLP protease subunit gene was ligated into the NotI and BamHI restricted plasmid pCA/Myc-His to produce plasmid pCACPNM909 (Figure 27).

20           The NotI/BamHI restricted PCR fragment containing the transglycolase/transpeptidase gene was ligated into the NotI and BamHI restricted plasmid pCA/Myc-His to produce plasmid pCACPNM440 (Figure 28).

          The NotI/KpnI restricted PCR fragment containing the CLPc protease gene was ligated into the NotI and KpnI  
25 restricted plasmid pCA/Myc-His to produce plasmid pCACPNM459 (Figure 29).

          The NotI/BamHI restricted PCR fragment containing the Thioredoxin gene was ligated into the NotI and BamHI restricted  
30 plasmid pCA/Myc-His to produce plasmid pCACPNM708 (Figure 30).

Each of the resulting plasmids pCACPNM213, pCACPNM882, pCACPNM208, pCACPNM1096, pCACPNM1097, pCACPNM909, pCACPNM440, pCACPNM459 and pCACPNM708, was transferred by electroporation into *E. coli* XL-1 blue (Stratagene) which was  
5 grown in LB broth containing 50 µg/ml carbenicillin. The plasmid was isolated by the Endo Free Plasmid Giga Kit™ (Qiagen) large scale DNA purification system. DNA concentration was determined by absorbance at 260 nm and the plasmid was verified after gel electrophoresis and ethidium  
10 bromide staining by comparison to molecular weight standards. The 5' and 3' ends of the gene were verified by sequencing using a LiCor model 4000 L DNA sequencer and IRD-800 labelled primers.

### Example 3:

15 This example illustrates the immunization of mice to achieve protection against an intranasal challenge of *C. pneumoniae*.

It has been previously demonstrated (Yang et al. Infect. Immun. May 1993. 61(5):2037-40) that mice are  
20 susceptible to intranasal infection with different isolates of *C. pneumoniae*. Strain AR-39 (Grayston et al (1990) Journal of Infectious Diseases 161:618-625) was used in Balb/c mice as a challenge infection model to examine the capacity of *Chlamydia* gene products delivered as naked DNA to elicit a protective  
25 response against a sublethal *C. pneumoniae* lung infection. Protective immunity is defined as an accelerated clearance of pulmonary infection.

Groups of 7 to 9 week old male Balb/c mice (8 to 10 per group) were immunized intramuscularly (i.m.) plus  
30 intranasally (i.n.) with plasmid DNA containing each of the *C. pneumoniae* protein gene as described in Examples 1 and 2.

Saline or the plasmid vector lacking an inserted Chlamydial gene was given to groups of control animals.

For i.m. immunization, alternate left and right quadriceps were injected with 100µg of DNA in 50µl of PBS on three occasions at 0, 3 and 6 weeks. For i.n. immunization, anaesthetized mice were aspirated 50µl of PBS containing 50 µg DNA on three occasions at 0, 3 and 6 weeks. At week 8, immunized mice were inoculated i.n. with  $5 \times 10^5$  IFU of *C. pneumoniae*, strain AR39 in 100µl of SPG buffer to test their ability to limit the growth of a sublethal *C. pneumoniae* challenge.

Lungs were taken from mice at day 9 post-challenge and immediately homogenised in SPG buffer (7.5% sucrose, 5mM glutamate, 12.5mM phosphate pH7.5). The homogenate was stored frozen at -70°C until assay. Dilutions of the homogenate were assayed for the presence of infectious *Chlamydia* by inoculation onto monolayers of susceptible cells. The inoculum was centrifuged onto the cells at 3000rpm for 1 hour, then the cells were incubated for three days at 35°C in the presence of 1µg/ml cycloheximide. After incubation the monolayers were fixed with formalin and methanol then immunoperoxidase stained for the presence of Chlamydial inclusions using convalescent sera from rabbits infected with *C. pneumoniae* and metal-enhanced DAB as a peroxidase substrate.

#### 25 A. Immunization with pCACPNM213

Figure 31 and Table 1 show that mice immunized i.n. and i.m. with pCACPNM213 had chlamydial lung titers less than 60,000 in 3 of 6 cases at day 9 (mean 51,833) whereas the range of values for control mice sham immunized with saline was 34,200-377,800 IFU/lung (mean 141,450) at day 9. DNA immunisation per se was not responsible for the observed

protective effect since another plasmid DNA construct, pCACPNM102, failed to protect, with lung titers in immunised mice similar to those obtained for saline-immunized control mice (mean 153,283). The construct pCACPNM102 is identical to  
5 pCACPNM213 except that the nucleotide sequence encoding the putative ATP-binding cassette is replaced with a *C. pneumoniae* nucleotide sequence encoding an unrelated ATP Synthase Subunit I protein.

#### B. Immunization with pCACPNM882

10               Figure 32 and Table 3 show that mice immunized i.n. and i.m. with pCACPNM882 had chlamydial lung titers less than 73,000 in 4 of 6 cases at day 9 (mean 77,500) whereas the range of values for control mice sham immunized with saline was 56,000-424,000 IFU/lung (mean 186,291) at day 9. DNA  
15 immunisation per se was not responsible for the observed protective effect since another plasmid DNA construct, pCACPNM647, failed to protect, with lung titers in immunised mice similar to those obtained for saline-immunized control mice (mean 143,883). The construct pCACPNM647 is identical to  
20 pCACPNM882 except that the nucleotide sequence encoding the putative Secretory locus ORF is replaced with a *C. pneumoniae* nucleotide sequence encoding an unrelated substrate binding protein.

#### C. Immunization with pCACPNM208

25               Figure 33 and Table 4 show that mice immunized i.n. and i.m. with pCACPNM208 had chlamydial lung titers less than 67,000 in 4 of 6 cases at day 9 (mean 81,766) whereas the range of values for control mice sham immunized with saline was 56,000-424,100 IFU/lung (mean 186,291) at day 9. DNA  
30 immunisation per se was not responsible for the observed protective effect since another plasmid DNA construct, pCACPNM647, failed to protect, with lung titers in immunised

mice similar to those obtained for saline-immunized control mice (mean 143,883). The construct pCACPNM647 is identical to pCACPNM208 except that the nucleotide sequence encoding the putative Endopeptidase is replaced with a *C. pneumoniae* nucleotide sequence encoding an unrelated protein.

#### D. Immunization with pCACPNM1096

Figure 34 and Table 6 show that mice immunized i.n. and i.m. with pCACPNM1096 had chlamydial lung titers less than 30,000 in 5 of 6 cases at day 9 (mean 25,000) whereas the range of values for control mice sham immunized with saline was 51,300-170,000 IFU/lung (mean 105,150) at day 9. DNA immunisation *per se* was not responsible for the observed protective effect since another plasmid DNA construct, pCACPNM553, failed to protect, with lung titers in immunised mice similar to those obtained for saline-immunized control mice (mean 111,583). The construct pCACPNM553 is identical to pCACPNM1096 except that the nucleotide sequence encoding the putative Protease is replaced with a *C. pneumoniae* nucleotide sequence encoding an unrelated protease.

#### E. Immunization with pCACPNM1097

Figure 35 and Table 8 show that mice immunized i.n. and i.m. with pCACPNM1097 had chlamydial lung titers less than 51,000 in 4 of 6 cases at day 9 (mean 62,883) whereas the range of values for control mice sham immunized with saline was 90,000-242,100 IFU/lung (mean 166,287) at day 9. DNA immunisation *per se* was not responsible for the observed protective effect since another plasmid DNA construct, pCACPNM1061, failed to protect, with lung titers in immunised mice similar to those obtained for saline-immunized control mice (mean 148,566). The construct pCACPNM1061 is identical to pCACPNM1097 except that the nucleotide sequence encoding the

putative Metalloprotease is replaced with a *C. pneumoniae* nucleotide sequence encoding an unrelated zinc Metalloprotease.

#### F. Immunization with pCACPNM908

Figure 36 and Table 10 show that mice immunized i.n. and i.m. with pCACPNM908 had chlamydial lung titers less than 40,000 in 3 of 6 cases at day 9 (mean 68,333) whereas the range of values for control mice sham immunized with saline was 56,000-424,100 IFU/lung (mean 207,962) at day 9. DNA immunisation *per se* was not responsible for the observed protective effect since another plasmid DNA construct, pCACPNM569, failed to protect, with lung titers in immunised mice similar to those obtained for saline-immunized control mice (mean 215,600). The construct pCACPNM569 is identical to pCACPNM908 except that the nucleotide sequence encoding the putative CLP protease ATPase is replaced with a *C. pneumoniae* nucleotide sequence encoding an unrelated signal peptidase.

#### G. Immunization with pCACPNM909

Figure 37 and Table 12 show that mice immunized i.n. and i.m. with pCACPNM909 had chlamydial lung titers less than 85,000 in 5 of 6 cases at day 9 (mean 87,683) whereas the range of values for control mice sham immunized with saline was 56,000-424,100 IFU/lung (mean 207,962) at day 9. DNA immunisation *per se* was not responsible for the observed protective effect since another plasmid DNA construct, pCACPNM569, failed to protect, with lung titers in immunised mice similar to those obtained for saline-immunized control mice (mean 215,600). The construct pCACPNM569 is identical to pCACPNM909 except that the nucleotide sequence encoding the putative CLP protease subunit is replaced with a *C. pneumoniae* nucleotide sequence encoding an unrelated signal peptidase.



#### H. Immunization with pCACPNM440

Figure 38 and Table 14 show that mice immunized i.n. and i.m. with pCACPNM440 had chlamydial lung titers less than 98,000 in 4 of 6 cases at day 9 (mean 87,616) whereas the range of values for control mice sham immunized with saline was 56,000-424,100 IFU/lung (mean 186,291) at day 9. DNA immunisation *per se* was not responsible for the observed protective effect since another plasmid DNA construct, pCACPNM647 failed to protect, with lung titers in immunised mice similar to those obtained for saline-immunized control mice (mean 143,883). The construct pCACPNM647 is identical to pCACPNM440 except that the nucleotide sequence encoding the putative transglycolase /transpeptidase gene is replaced with a *C. pneumoniae* nucleotide sequence encoding an unrelated gene.

#### I. Immunization with pCACPNM459

Figure 39 and Table 16 show that mice immunized i.n. and i.m. with pCACPNM459 had chlamydial lung titers less than 70,000 in 4 of 6 cases at day 9 (mean 70,516) whereas the range of values for control mice sham immunized with saline was 56,000-424,100 IFU/lung (mean 186,291) at day 9. DNA immunisation *per se* was not responsible for the observed protective effect since another plasmid DNA construct, pCACPNM647, failed to protect, with lung titers in immunised mice similar to those obtained for saline-immunized control mice (mean 143,883). The construct pCACPNM647 is identical to pCACPNM459 except that the nucleotide sequence encoding the putative CLPc protease is replaced with a *C. pneumoniae* nucleotide sequence encoding an unrelated gene.

#### J. Immunization with pCACPNM708

Figure 40 and Table 18 show that mice immunized i.n. and i.m. with pCACPNM708 had chlamydial lung titers less than

52,000 in 4 of 6 cases at day 9 (mean 73,916) whereas the range of values for control mice sham immunized with saline was 56,000-424,100 IFU/lung (mean 207,962) at day 9. DNA immunisation *per se* was not responsible for the observed protective effect since another plasmid DNA construct, pCACPNM569, failed to protect, with lung titers in immunised mice similar to those obtained for saline-immunized control mice (mean 215,600). The construct pCACPNM569 is identical to pCACPNM708 except that the nucleotide sequence encoding the putative thioredoxin is replaced with a *C. pneumoniae* nucleotide sequence encoding an unrelated *C. pneumoniae* gene.

Example 4:

This example illustrates the identification of B- and T-cell epitopes in proteins as expressed from each of pCACPNM213, pCACPNM882, pCACPNM208, pCACPNM1096, pCACPNM1097, pCACPNM909, pCACPNM440, pCACPNM459 and pCACPNM708.

B-cell epitopes were identified based on the product of flexibility and hydrophobicity propensities using the program SEQSEE (Wishart DS, et al. "SEQSEE: a comprehensive program suite for protein sequence analysis." *Comput Appl Biosci.* 1994 Apr;10(2):121-32) to identify external surface features (epitopes). T-cell epitopes for HLA-A0201 MHC subclass were identified based on the algorithm of Parker et al. 1995 (Parker KC, et al. "Peptide binding to MHC class I molecules: implications for antigenic peptide prediction." *Immunol Res* 1995;14(1):34-57). These epitopes are shown in Tables 2, 5, 7, 9, 11, 13, 15, 17 and 19 and SEQ ID NOs: 41 to 74.

**Table 1**

MOUSE	BACTERIAL LOAD (INCLUSION FORMING UNITS PER LUNG) IN THE LUNGS OF BALB/C MICE IMMUNIZED WITH VARIOUS DNA IMMUNIZATION CONSTRUCTS		
	IMMUNIZING CONSTRUCT		
	Saline	pCACP NM102	pCACP NM213
	Day 9	Day 9	Day 9
1	64900	207500	54200
2	116500	166500	10600
3	34200	114700	67400
4	377800	167400	32000
5	86200	179700	66900
6	206200	83900	79900
7	142600		
8	103200		
MEAN	141450	153283.333	51833.3333
SD	108598.7	45417.99	25908.35
Wilcoxon p		1.655	0.0293

**Table 2: Identified B- T-cell epitopes from CPNM213**

B cell epitope	T cell epitope
188 VHHTLRESYKKGTPPST (SEQ ID No: 41)	434 WIAEYVSPV (SEQ ID No: 43)
345 NLQKEISTEERQTKAR (SEQ ID No: 42)	

**Table 3**

MOUSE	BACTERIAL LOAD (INCLUSION FORMING UNITS PER LUNG) IN THE LUNGS OF BALB/C MICE IMMUNIZED WITH VARIOUS DNA IMMUNIZATION CONSTRUCTS		
	IMMUNIZING CONSTRUCT		
	Saline	pCACPNM647	pCACPNM882
	Day 9	Day 9	Day 9
1	209800	45100	18100
2	70000	222000	130300
3	226700	152500	72900
4	178900	89000	53500
5	424100	95500	63400
6	242200	259200	126800
7	256000		
8	56000		
9	173600		
10	185000		
11	121400		
12	91800		
MEAN	186291.667	143883.333	77500
SD	100263.3	83169.31	43686.75
Wilcoxon p		0.4936	0.0182

**Table 4**

MOUSE	BACTERIAL LOAD (INCLUSION FORMING UNITS PER LUNG) IN THE LUNGS OF BALB/C MICE IMMUNIZED WITH VARIOUS DNA IMMUNIZATION CONSTRUCTS		
	IMMUNIZING CONSTRUCT		
	Saline	pCACPNM647	pCACPNM208
	Day 9	Day 9	Day 9
1	209800	45100	142500
2	70000	222000	66900
3	226700	152500	58200
4	178900	89000	46500
5	424100	95500	110900
6	242200	259200	65600
7	256000		
8	56000		
9	173600		
10	185000		
11	121400		
12	91800		
MEAN	186291.667	143883.333	81766.6667
SD	100263.3	83169.31	36929.10
Wilcoxon p		0.4936	0.0135

**Table 5 Identified B- T-cell epitopes from CPNM208**

B cell epitope	T cell epitope
220 KGNSSPRSPAP (SEQ ID No: 44)	67 LLIEDMDLI (SEQ ID No: 46)
313 GENFQKNSS (SEQ ID No: 45)	66 NLLIEDMDL (SEQ ID No: 47)

**Table 6**

MOUSE	BACTERIAL LOAD (INCLUSION FORMING UNITS PER LUNG) IN THE LUNGS OF BALB/C MICE IMMUNIZED WITH VARIOUS DNA IMMUNIZATION CONSTRUCTS		
	IMMUNIZING CONSTRUCT		
	Saline	pCACPNM553	pCACPNM1096
	Day 9	Day 9	Day 9
1	136900	135600	21000
2	81700	112600	9700
3	119400	88600	28500
4	58500	121700	52000
5	110600	165300	17200
6	51300	45700	21600
7	170000		
8	112800		
MEAN	105150	111583.333	25000
SD	39876.3	41071.91	14585.88
Wilcoxon p		1.245	0.0013

**Table 7 Identified B- T-cell epitopes from CPNM1096**

B cell epitope	T cell epitope
328 TDLEGLEEDHKDSPWE (SEQ ID No: 48)	135 YLGDEILEV (SEQ ID No: 50)
589 SENAKKSEEQTSPQETPE (SEQ ID No: 49)	373 YLYSLLSML (SEQ ID No: 51)

**Table 8**

MOUSE	BACTERIAL LOAD (INCLUSION FORMING UNITS PER LUNG) IN THE LUNGS OF BALB/C MICE IMMUNIZED WITH VARIOUS DNA IMMUNIZATION CONSTRUCTS		
	IMMUNIZING CONSTRUCT		
	Saline	pCACPNM106 1	pCACPNM1097
	Day 9	Day 9	Day 9
1	232900	120800	50300
2	168100	184100	43900
3	105500	95600	65200
4	173100	147500	157900
5	90000	218700	22800
6	242100	124700	37200
7	183700		
8	134900		
MEAN	166287.5	148566.667	62883.3333
SD	54821.4	45450.00	48618.00
Wilcoxon p		0.662	0.0047

**Table 9 Identified B- T-cell epitopes from CPNM1097**

B cell epitope	T cell epitope
198 TTNRQKAL (SEQ ID No: 52)	207 SVLSRVNYV (SEQ ID No: 54)
221 VNSSNSNRLRE (SEQ ID No: 53)	279 KLSSLIPGL (SEQ ID No: 55)
	118 ILIGHKKHV (SEQ ID No: 56)

**Table 10**

MOUSE	BACTERIAL LOAD (INCLUSION FORMING UNITS PER LUNG) IN THE LUNGS OF BALB/C MICE IMMUNIZED WITH VARIOUS DNA IMMUNIZATION CONSTRUCTS		
	IMMUNIZING CONSTRUCT		
	Saline	pCACPNM569	pCACPNM908
	Day 9	Day 9	Day 9
1	209800	142800	37300
2	70000	420700	85000
3	226700	116600	35700
4	178900	161300	39700
5	424100	89200	123400
6	242200	363000	88900
7	256000		
8	56000		
MEAN	207962.5	215600	68333.3333
SD	115585.8	139870.70	36279.40
Wilcoxon p		0.8518	0.02

**Table 11 Identified B- T-cell epitopes from CPNM908**

B cell epitope	T cell epitope
226 PPKGGRKHPNQEYI (SEQ ID No: 57)	137 KILDVPFTI (SEQ ID No: 59)
273 SDDQADLSQKTRDH (SEQ ID No: 58)	168 LLQAADYDV (SEQ ID No: 60)



**Table 12**

MOUSE	BACTERIAL LOAD (INCLUSION FORMING UNITS PER LUNG) IN THE LUNGS OF BALB/C MICE IMMUNIZED WITH VARIOUS DNA IMMUNIZATION CONSTRUCTS		
	IMMUNIZING CONSTRUCT		
	Saline	pCACPNM569	PCACPNM909
	Day 9	Day 9	Day 9
1	209800	142800	206700
2	70000	420700	84700
3	226700	116600	81100
4	178900	161300	56700
5	424100	89200	53900
6	242200	363000	43000
7	256000		
8	56000		
MEAN	207962.5	215600	87683.3333
SD	115585.8	139870.70	60522.87
Wilcoxon p		0.8518	0.0426

**Table 13 Identified B- T-cell epitopes from CPNM909**

B cell epitope	T cell epitope
107 GTKGKRHAL (SEQ ID No: 61)	76 AIYDTIRFL (SEQ ID No: 63)
193 AKETNKDTSST (SEQ ID No: 62)	

**Table 14**

MOUSE	BACTERIAL LOAD (INCLUSION FORMING UNITS PER LUNG) IN THE LUNGS OF BALB/C MICE IMMUNIZED WITH VARIOUS DNA IMMUNIZATION CONSTRUCTS		
	IMMUNIZING CONSTRUCT		
	Saline	pCACPNM647	pCACPNM440
	Day 9	Day 9	Day 9
1	209800	45100	97200
2	70000	222000	92500
3	226700	152500	104400
4	178900	89000	60900
5	424100	95500	40400
6	242200	259200	130300
7	256000		
8	56000		
9	173600		
10	185000		
11	121400		
12	91800		
MEAN	186291.667	143883.333	87616.6667
SD	100263.3	83169.31	32132.31
Wilcoxon p		0.4936	0.0415

**Table 15 Identified B- T-cell epitopes from CPNM440**

B cell epitope	T cell epitope
287 DPTNYKEYFNNKERIEHTK (SEQ ID No: 64)	40 ALGQHEFCV (SEQ ID No: 66)
637 KRLYEEWNRSPKQGGTR (SEQ ID No: 65)	456 ILATGIQMV (SEQ ID No: 67)

**Table 16**

MOUSE	BACTERIAL LOAD (INCLUSION FORMING UNITS PER LUNG) IN THE LUNGS OF BALB/C MICE IMMUNIZED WITH VARIOUS DNA IMMUNIZATION CONSTRUCTS		
	IMMUNIZING CONSTRUCT		
	Saline	pCACPNM647	pCACPNM459
	Day 9	Day 9	Day 9
1	209800	45100	77400
2	70000	222000	60700
3	226700	152500	121000
4	178900	89000	68500
5	424100	95500	44800
6	242200	259200	50700
7	256000		
8	56000		
9	173600		
10	185000		
11	121400		
12	91800		
MEAN	186291.667	143883.333	70516.6667
SD	100263.3	83169.31	27387.69
Wilcoxon p		0.4936	0.0047

**Table 17 Identified B- T-cell epitopes from CPNM459**

B cell epitope	T cell epitope
467 DEEKKLRERLQSMKQEWENHKEEHQ (SEQ ID No: 68)	565 FLFLGPTGV (SEQ ID No: 70)
548 IRRSRTGIKDPNRPTG (SEQ ID No: 69)	410 FLDPKAIDL (SEQ ID No: 71)

**Table 18**

MOUSE	BACTERIAL LOAD (INCLUSION FORMING UNITS PER LUNG) IN THE LUNGS OF BALB/C MICE IMMUNIZED WITH VARIOUS DNA IMMUNIZATION CONSTRUCTS		
	IMMUNIZING CONSTRUCT		
	Saline	pCACPNM569	pCACPNM708
	Day 9	Day 9	Day 9
1	209800	142800	95100
2	70000	420700	189600
3	226700	116600	29000
4	178900	161300	51400
5	424100	89200	31500
6	242200	363000	46900
7	256000		
8	56000		
MEAN	207962.5	215600	73916.6667
SD	115585.8	139870.70	61457.22
Wilcoxon p		0.8518	0.0127

**Table 19 Identified B- T-cell epitopes from pCPNM708**

B cell epitope	T cell epitope
54 NIDENSKPAETYE (SEQ ID No: 72)	40 NLAAELPHV (SEQ ID No: 73)
	74 ILFKDGNEV (SEQ ID No: 74)

CLAIMS:

1. A vaccine comprising a vaccine vector and at least one first nucleic acid selected from any one of:

(i) a nucleic acid sequence set forth in any one of  
5 SEQ ID Nos: 1, 3, 5, 7, 9, 11, 13, 15, 17 and 19;

(ii) a nucleic acid sequence which encodes a polypeptide encoded by any one of SEQ ID Nos: 1, 3, 5, 7, 9, 11, 13, 15, 17 and 19;

(iii) a nucleic acid sequence which encodes a  
10 polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by any one of SEQ ID Nos: 1, 3, 5, 7, 9, 11, 13, 15, 17 and 19; and

(iv) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in any one of SEQ ID  
15 Nos: 2, 4, 6, 8, 10, 12, 14, 16, 18 and 20;

(v) a nucleic acid sequence as defined in (i), (ii) or (iv), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid  
20 sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iv);

wherein each first nucleic acid is capable of being expressed.

2. A vaccine comprising a vaccine vector and at least  
25 one first nucleic acid selected from any one of:

(i) a nucleic acid sequence comprising at least 36 consecutive nucleotides from any one of SEQ ID Nos: 1, 3, 5, 7, 9, 11, 13, 15, 17 and 19;

(ii) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino acids from any one of SEQ ID Nos: 2, 4, 6, 8, 10, 12, 14, 16, 18 and 20;

5 (iii) a nucleic acid sequence as defined in (i) or (ii), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding fragment of (i) or (ii);

10 wherein each first nucleic acid is capable of being expressed.

3. A vaccine comprising a vaccine vector and at least one first nucleic acid selected from any one of:

(i) SEQ ID No: 1;

15 (ii) a nucleic acid sequence which encodes a polypeptide encoded by SEQ ID No: 1;

(iii) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by SEQ ID No: 1; and

20 (iv) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in SEQ ID No: 2;

(v) a nucleic acid sequence as defined in (i), (ii) or (iv), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains  
25 immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iv);

wherein each first nucleic acid is capable of being expressed.

4. A vaccine comprising a vaccine vector and at least one first nucleic acid selected from any one of:

(i) a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 1;

5 (ii) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 2;

(iii) a nucleic acid sequence as defined in (i) or (ii), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding fragment of (i) or (ii);

wherein each first nucleic acid is capable of being expressed.

15 5. A vaccine comprising a vaccine vector and at least one first nucleic acid encoding a fusion protein, wherein the fusion protein comprises:

(a) a first polypeptide encoded by a nucleic acid selected from any one of:

20 (i) SEQ ID No: 1;

(ii) a nucleic acid sequence which encodes a polypeptide encoded by SEQ ID No: 1;

(iii) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by SEQ ID No: 1; and

25 (iv) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in SEQ ID No: 2;

(v) a nucleic acid sequence as defined in (i), (ii) or (iv), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iv); and

(b) a second polypeptide;

wherein each first nucleic acid is capable of being expressed.

6. A vaccine comprising a vaccine vector and at least one first nucleic acid encoding a fusion protein, wherein the fusion protein comprises:

(a) a first polypeptide encoded by a nucleic acid selected from any one of:

(i) a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 1;

(ii) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 2;

(iii) a nucleic acid sequence as defined in (i) or (ii), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding fragment of (i) or (ii); and

(b) a second polypeptide;

wherein each first nucleic acid is capable of being expressed.

7. The vaccine of claim 5 or 6 wherein the second polypeptide is a heterologous signal peptide.



8. The vaccine of claim 5 or 6 wherein the second polypeptide has adjuvant activity.
9. The vaccine of any one of claims 3 to 8 wherein wherein each first nucleic acid is operatively linked to one or  
5 more expression control sequences.
10. A vaccine according to any one of claims 3 to 9, further comprising a second nucleic acid encoding an additional polypeptide which enhances the immune response to the polypeptide expressed by the first nucleic acid.
- 10 11. The vaccine of claim 10 wherein the second nucleic acid encodes an additional *Chlamydia* polypeptide.
12. A pharmaceutical composition comprising a vaccine according to any one of claims 3 to 11 and a pharmaceutically acceptable carrier.
- 15 13. A fusion protein comprising a first and a second polypeptide, wherein the first polypeptide is selected from any one of:
- (i) a polypeptide encoded by SEQ ID NO: 1;
  - (ii) a polypeptide which is at least 75% identical in  
20 amino acid sequence to SEQ ID NO: 2 or to the polypeptide encoded by SEQ ID NO: 1;
  - (iii) a polypeptide of SEQ ID NO: 2; and
  - (iv) a polypeptide as defined in (i), (ii) or (iii) which has been modified without loss of immunogenicity and is  
25 at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iii).

14. A fusion protein comprising a first and a second polypeptide, wherein the first polypeptide is selected from any one of:

(i) a polypeptide encoded by a nucleic acid sequence  
5 comprising at least 36 consecutive nucleotides from SEQ ID NO:  
1;

(ii) a polypeptide which is an immunogenic fragment  
comprising at least 12 consecutive amino acids from SEQ ID No:  
2;

10 (iii) a polypeptide as defined in (i) or (ii), which  
has been modified without loss of immunogenicity and is at  
least 75% identical in amino acid sequence to the corresponding  
polypeptide of (i) or (ii).

15 15. The fusion protein of claim 13 or 14 wherein the  
second polypeptide is a heterologous signal peptide.

16. The fusion protein of claim 13 or 14 wherein the  
second polypeptide has adjuvant activity.

17. An antibody against the fusion protein of any one of  
claims 13 to 15.

20 18. A vaccine comprising at least one first polypeptide  
selected from any one of:

(i) a polypeptide encoded by SEQ ID NO: 1;

(ii) a polypeptide which is at least 75% identical in  
amino acid sequence to SEQ ID NO: 2 or to the polypeptide  
25 encoded by SEQ ID NO: 1;

(iii) a polypeptide of SEQ ID NO: 2; and

(iv) a polypeptide as defined in (i), (ii) or (iii) which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i),  
5 (ii) or (iii).

19. A vaccine comprising at least one first polypeptide selected from any one of:

(i) a polypeptide encoded by a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO:  
10 1;

(ii) a polypeptide which is an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No:  
2;

(iii) a polypeptide as defined in (i) or (ii), which  
15 has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) or (ii).

20. A vaccine comprising at least one fusion protein, wherein the fusion protein comprises a first and a second  
20 polypeptide, wherein the first polypeptide is selected from any one of:

(i) a polypeptide encoded by SEQ ID NO: 1;

(ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 2 or to the polypeptide  
25 encoded by SEQ ID NO: 1;

(iii) a polypeptide of SEQ ID NO: 2; and

(iv) a polypeptide as defined in (i), (ii) or (iii) which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the

corresponding polypeptide encoded by the nucleic acid of (i),  
(ii) or (iii).

21. A vaccine comprising at least one fusion protein,  
wherein the fusion protein comprises a first and a second  
5 polypeptide, wherein the first polypeptide is selected from any  
one of:

(i) a polypeptide encoded by a nucleic acid sequence  
comprising at least 36 consecutive nucleotides from SEQ ID NO:  
1;

10 (ii) a polypeptide which is an immunogenic fragment  
comprising at least 12 consecutive amino acids from SEQ ID No:  
2;

(iii) a polypeptide as defined in (i) or (ii), which  
has been modified without loss of immunogenicity and is at  
15 least 75% identical in amino acid sequence to the corresponding  
polypeptide of (i) or (ii).

22. The vaccine of claim 20 or 21 wherein the second  
polypeptide is a heterologous signal peptide.

23. The vaccine of claim 20 or 21 wherein the second  
20 polypeptide has adjuvant activity.

24. A vaccine according to any one of claims 18 to 23,  
further comprising an additional polypeptide which enhances the  
immune response to the first polypeptide.

25. The vaccine according to claim 24 wherein the  
25 additional polypeptide comprises a *Chlamydia* polypeptide.

26. A pharmaceutical composition comprising a vaccine  
according to any one of claims 18 to 25 and a pharmaceutically  
acceptable carrier.

27. A pharmaceutical composition comprising an antibody according to claim 17 and a pharmaceutically acceptable carrier.
28. A method for preventing or treating *Chlamydia* infection comprising administering to a mammal an effective amount of the vaccine of any one of claims 3 to 11 and 18 to 25.
29. A method for preventing or treating *Chlamydia* infection comprising administering to a mammal an effective amount of the composition of any one of claims 12, 26 and 27.
30. A method for preventing or treating *Chlamydia* infection comprising administering to a mammal an effective amount of the fusion protein of any one of claims 13 to 16.
31. A method for preventing or treating *Chlamydia* infection comprising administering to a mammal an effective amount of the antibody of claim 17.
32. A commercial package comprising at least one nucleic acid selected from any one of:
- (i) SEQ ID No: 1;
  - (ii) a nucleic acid sequence which encodes a polypeptide encoded by SEQ ID No: 1;
  - (iii) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by SEQ ID No: 1; and
  - (iv) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in SEQ ID No: 2;
  - (v) a nucleic acid sequence as defined in (i), (ii) or (iv), which has been modified to encode a modified

polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iv);

- 5 wherein each first nucleic acid is capable of being expressed; and instructions for use in eliciting an immunoprotective response in a mammal.

33. A commercial package comprising at least one nucleic acid selected from any one of:

- 10 (i) a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 1;

(ii) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 2;

- 15 (iii) a nucleic acid sequence as defined in (i) or (ii), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding fragment of (i) or (ii);

- 20 wherein each first nucleic acid is capable of being expressed; and

instructions for use in eliciting an immunoprotective response in a mammal.

34. A commercial package comprising at least one  
25 polypeptide selected from any one of:

(i) a polypeptide encoded by SEQ ID NO: 1;

(ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 2 or to the polypeptide encoded by SEQ ID NO: 1;

(iii) a polypeptide of SEQ ID NO: 2; and

5           (iv) a polypeptide as defined in (i), (ii) or (iii) which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iii);

10 and instructions for use in eliciting an immunoprotective response in a mammal.

35.           A commercial package comprising at least one polypeptide selected from any one of:

              (i) a polypeptide encoded by a nucleic acid sequence  
15 comprising at least 36 consecutive nucleotides from SEQ ID NO: 1;

              (ii) a polypeptide which is an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 2;

20           (iii) a polypeptide as defined in (i) or (ii), which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) or (ii);

and instructions for use in eliciting an immunoprotective  
25 response in a mammal.

36.           Expression plasmid pCACPNM213 as shown in Figure 21.

37.           A vaccine comprising a vaccine vector and at least one first nucleic acid selected from:

(i) a nucleic acid encoding a polypeptide of any one of SEQ ID Nos: 41 to 43; and

(ii) a nucleic acid sequence as defined in (i) which has been modified to encode a modified conservatively substituted polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i).

38. A vaccine comprising a vaccine vector and at least one first polypeptide selected from:

(i) a polypeptide of any one of SEQ ID Nos: 41 to 43; and

(ii) a polypeptide as defined in (i) which has been modified by conservative substitution, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i).

39. A vaccine comprising a vaccine vector and at least one first nucleic acid selected from any one of:

(i) SEQ ID No: 3;

(ii) a nucleic acid sequence which encodes a polypeptide encoded by SEQ ID No: 3;

(iii) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by SEQ ID No: 3; and

(iv) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in SEQ ID No: 4;



(v) a nucleic acid sequence as defined in (i), (ii) or (iv), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iv);

wherein each first nucleic acid is capable of being expressed.

40. A vaccine comprising a vaccine vector and at least one first nucleic acid selected from any one of:

(i) a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 3;

(ii) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 4;

(iii) a nucleic acid sequence as defined in (i) or (ii), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding fragment of (i) or (ii);

wherein each first nucleic acid is capable of being expressed.

41. A vaccine comprising a vaccine vector and at least one first nucleic acid encoding a fusion protein, wherein the fusion protein comprises:

(a) a first polypeptide encoded by a nucleic acid selected from any one of:

(i) SEQ ID No: 3;

(ii) a nucleic acid sequence which encodes a polypeptide encoded by SEQ ID No: 3;

(iii) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid  
5 sequence to the polypeptide encoded by SEQ ID No: 3; and

(iv) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in SEQ ID No: 4;

(v) a nucleic acid sequence as defined in (i), (ii) or (iv), which has been modified to encode a modified  
10 polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iv); and

(b) a second polypeptide;

15 wherein each first nucleic acid is capable of being expressed.

42. A vaccine comprising a vaccine vector and at least one first nucleic acid encoding a fusion protein, wherein the fusion protein comprises:

(a) a first polypeptide encoded by a nucleic acid  
20 selected from any one of:

(i) a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 3;

(ii) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino  
25 acids from SEQ ID No: 4;

(iii) a nucleic acid sequence as defined in (i) or (ii), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is

at least 75% identical in amino acid sequence to the corresponding fragment of (i) or (ii); and

(b) a second polypeptide;

wherein each first nucleic acid is capable of being  
5 expressed.

43. The vaccine of claim 41 or 42 wherein the second polypeptide is a heterologous signal peptide.

44. The vaccine of claim 41 or 42 wherein the second polypeptide has adjuvant activity.

10 45. The vaccine of any one of claims 39 to 44 wherein wherein each first nucleic acid is operatively linked to one or more expression control sequences.

46. A vaccine according to any one of claims 39 to 45, further comprising a second nucleic acid encoding an additional  
15 polypeptide which enhances the immune response to the polypeptide expressed by the first nucleic acid.

47. The vaccine of claim 46 wherein the second nucleic acid encodes an additional *Chlamydia* polypeptide.

48. A pharmaceutical composition comprising a vaccine  
20 according to any one of claims 39 to 47 and a pharmaceutically acceptable carrier.

49. A fusion protein comprising a first and a second polypeptide, wherein the first polypeptide is selected from any one of:

25 (i) a polypeptide encoded by SEQ ID NO: 3;

(ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 4 or to the polypeptide encoded by SEQ ID NO: 3;

(iii) a polypeptide of SEQ ID NO: 4; and

5 (iv) a polypeptide as defined in (i), (ii) or (iii) which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iii).

10 50. A fusion protein comprising a first and a second polypeptide, wherein the first polypeptide is selected from any one of:

(i) a polypeptide encoded by a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO:  
15 3;

(ii) a polypeptide which is an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 4;

(iii) a polypeptide as defined in (i) or (ii), which  
20 has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) or (ii).

51. The fusion protein of claim 49 or 50 wherein the second polypeptide is a heterologous signal peptide.

25 52. The fusion protein of claim 49 or 50 wherein the second polypeptide has adjuvant activity.

53. An antibody against the fusion protein of any one of claims 49 to 51.

54. A vaccine comprising at least one first polypeptide selected from any one of:

(i) a polypeptide encoded by SEQ ID NO: 3;

(ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 4 or to the polypeptide encoded by SEQ ID NO: 3;

(iii) a polypeptide of SEQ ID NO: 4; and

(iv) a polypeptide as defined in (i), (ii) or (iii) which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iii).

55. A vaccine comprising at least one first polypeptide selected from any one of:

(i) a polypeptide encoded by a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 3;

(ii) a polypeptide which is an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 4;

(iii) a polypeptide as defined in (i) or (ii), which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) or (ii).

56. A vaccine comprising at least one fusion protein, wherein the fusion protein comprises a first and a second polypeptide, wherein the first polypeptide is selected from any one of:

(i) a polypeptide encoded by SEQ ID NO: 3;

(ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 4 or to the polypeptide encoded by SEQ ID NO: 3;

5 (iii) a polypeptide of SEQ ID NO: 4; and

(iv) a polypeptide as defined in (i), (ii) or (iii) which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i),  
10 (ii) or (iii).

57. A vaccine comprising at least one fusion protein, wherein the fusion protein comprises a first and a second polypeptide, wherein the first polypeptide is selected from any one of:

15 (i) a polypeptide encoded by a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 3;

(ii) a polypeptide which is an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No:  
20 4;

(iii) a polypeptide as defined in (i) or (ii), which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) or (ii).

25 58. The vaccine of claim 56 or 57 wherein the second polypeptide is a heterologous signal peptide.

59. The vaccine of claim 56 or 57 wherein the second polypeptide has adjuvant activity.

60. A vaccine according to any one of claims 54 or 59, further comprising an additional polypeptide which enhances the immune response to the first polypeptide.
61. The vaccine according to claim 60 wherein the  
5 additional polypeptide comprises a *Chlamydia* polypeptide.
62. A pharmaceutical composition comprising a vaccine according to any one of claims 54 to 61 and a pharmaceutically acceptable carrier.
63. A pharmaceutical composition comprising an antibody  
10 according to claim 53 and a pharmaceutically acceptable carrier.
64. A method for preventing or treating *Chlamydia* infection comprising administering to a mammal an effective amount of the vaccine of any one of claims 39 to 47 and 54 to  
15 61.
65. A method for preventing or treating *Chlamydia* infection comprising administering to a mammal an effective amount of the composition of any one of claims 48, 62 and 63.
66. A method for preventing or treating *Chlamydia*  
20 infection comprising administering to a mammal an effective amount of the fusion protein of any one of claims 49 to 52.
67. A method for preventing or treating *Chlamydia* infection comprising administering to a mammal an effective amount of the antibody of claim 53.
- 25 68. A commercial package comprising at least one nucleic acid selected from any one of:

(i) SEQ ID No: 3;

(ii) a nucleic acid sequence which encodes a polypeptide encoded by SEQ ID No: 3;

(iii) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid  
5 sequence to the polypeptide encoded by SEQ ID No: 3; and

(iv) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in SEQ ID No: 4;

(v) a nucleic acid sequence as defined in (i), (ii) or (iv), which has been modified to encode a modified  
10 polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iv);

wherein each first nucleic acid is capable of being  
15 expressed; and

instructions for use in eliciting an immunoprotective response in a mammal.

69. A commercial package comprising at least one nucleic acid selected from any one of:

20 (i) a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 3;

(ii) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 4;

25 (iii) a nucleic acid sequence as defined in (i) or (ii), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding fragment of (i) or (ii);



wherein each first nucleic acid is capable of being expressed; and

instructions for use in eliciting an immunoprotective response in a mammal.

5 70. A commercial package comprising at least one polypeptide selected from any one of:

(i) a polypeptide encoded by SEQ ID NO: 3;

(ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 4 or to the polypeptide  
10 encoded by SEQ ID NO: 3;

(iii) a polypeptide of SEQ ID NO: 4; and

(iv) a polypeptide as defined in (i), (ii) or (iii) which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the  
15 corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iii); and

instructions for use in eliciting an immunoprotective response in a mammal.

71. A commercial package comprising at least one  
20 polypeptide selected from any one of:

(i) a polypeptide encoded by a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 3;

(ii) a polypeptide which is an immunogenic fragment  
25 comprising at least 12 consecutive amino acids from SEQ ID No: 4;

(iii) a polypeptide as defined in (i) or (ii), which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) or (ii);

5 and instructions for use in eliciting an immunoprotective response in a mammal.

72. Expression plasmid pCACPNM882 as shown in Figure 22.

73. A vaccine comprising a vaccine vector and at least one first nucleic acid selected from any one of:

10 (i) SEQ ID No: 5;

(ii) a nucleic acid sequence which encodes a polypeptide encoded by SEQ ID No: 5;

(iii) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid  
15 sequence to the polypeptide encoded by SEQ ID No: 5; and

(iv) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in SEQ ID No: 6;

(v) a nucleic acid sequence as defined in (i), (ii) or (iv), which has been modified to encode a modified  
20 polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iv);

wherein each first nucleic acid is capable of being  
25 expressed.

74. A vaccine comprising a vaccine vector and at least one first nucleic acid selected from any one of:

(i) a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 5;

(ii) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 6;

(iii) a nucleic acid sequence as defined in (i) or (ii), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding fragment of (i) or (ii);

wherein each first nucleic acid is capable of being expressed.

75. A vaccine comprising a vaccine vector and at least one first nucleic acid encoding a fusion protein, wherein the fusion protein comprises:

(a) a first polypeptide encoded by a nucleic acid selected from any one of:

(i) SEQ ID No: 5;

(ii) a nucleic acid sequence which encodes a polypeptide encoded by SEQ ID No: 5;

(iii) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by SEQ ID No: 5; and

(iv) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in SEQ ID No: 6;

(v) a nucleic acid sequence as defined in (i), (ii) or (iv), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains

immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iv); and

(b) a second polypeptide;

5 wherein each first nucleic acid is capable of being expressed.

76. A vaccine comprising a vaccine vector and at least one first nucleic acid encoding a fusion protein, wherein the fusion protein comprises:

(a) a first polypeptide encoded by a nucleic acid  
10 selected from any one of:

(i) a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 5;

(ii) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino  
15 acids from SEQ ID No: 6;

(iii) a nucleic acid sequence as defined in (i) or (ii), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the  
20 corresponding fragment of (i) or (ii); and

(b) a second polypeptide;

wherein each first nucleic acid is capable of being expressed.

77. The vaccine of claim 75 or 76 wherein the second  
25 polypeptide is a heterologous signal peptide.

78. The vaccine of claim 75 or 76 wherein the second polypeptide has adjuvant activity.

79. The vaccine of any one of claims 73 to 78 wherein each first nucleic acid is operatively linked to one or more expression control sequences.

80. A vaccine according to any one of claims 73 to 5 79, further comprising a second nucleic acid encoding an additional polypeptide which enhances the immune response to the polypeptide expressed by the first nucleic acid.

81. The vaccine of claim 80 wherein the second nucleic acid encodes an additional *Chlamydia* polypeptide.

10 82. A pharmaceutical composition comprising a vaccine according to any one of claims 73 to 81 and a pharmaceutically acceptable carrier.

83. A fusion protein comprising a first and a second polypeptide, wherein the first polypeptide is selected from any 15 one of:

(i) a polypeptide encoded by SEQ ID NO: 5;

(ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 6 or to the polypeptide encoded by SEQ ID NO: 5;

20 (iii) a polypeptide of SEQ ID NO: 6; and

(iv) a polypeptide as defined in (i), (ii) or (iii) which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), 25 (ii) or (iii).

84. A fusion protein comprising a first and a second polypeptide, wherein the first polypeptide is selected from any one of:

(i) a polypeptide encoded by a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 5;

(ii) a polypeptide which is an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 6;

(iii) a polypeptide as defined in (i) or (ii), which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) or (ii).

85. The fusion protein of claim 83 or 84 wherein the second polypeptide is a heterologous signal peptide.

86. The fusion protein of claim 83 or 84 wherein the second polypeptide has adjuvant activity.

87. An antibody against the fusion protein of any one of claims 83 to 85.

88. A vaccine comprising at least one first polypeptide selected from any one of:

(i) a polypeptide encoded by SEQ ID NO: 5;

(ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 6 or to the polypeptide encoded by SEQ ID NO: 5;

(iii) a polypeptide of SEQ ID NO: 6; and

(iv) a polypeptide as defined in (i), (ii) or (iii) which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iii).

89. A vaccine comprising at least one first polypeptide selected from any one of:

(i) a polypeptide encoded by a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO:  
5 5;

(ii) a polypeptide which is an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No:  
6;

(iii) a polypeptide as defined in (i) or (ii), which  
10 has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) or (ii).

90. A vaccine comprising at least one fusion protein, wherein the fusion protein comprises a first and a second  
15 polypeptide, wherein the first polypeptide is selected from any one of:

(i) a polypeptide encoded by SEQ ID NO: 5;

(ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 6 or to the polypeptide  
20 encoded by SEQ ID NO: 5;

(iii) a polypeptide of SEQ ID NO: 6; and

(iv) a polypeptide as defined in (i), (ii) or (iii) which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the  
25 corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iii).

91. A vaccine comprising at least one fusion protein, wherein the fusion protein comprises a first and a second

polypeptide, wherein the first polypeptide is selected from any one of:

(i) a polypeptide encoded by a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO:

5 5;

(ii) a polypeptide which is an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 6;

(iii) a polypeptide as defined in (i) or (ii), which  
10 has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) or (ii).

92. The vaccine of claim 90 or 91 wherein the second polypeptide is a heterologous signal peptide.

15 93. The vaccine of claim 90 or 91 wherein the second polypeptide has adjuvant activity.

94. A vaccine according to any one of claims 88 to 93, further comprising an additional polypeptide which enhances the immune response to the first polypeptide.

20 95. The vaccine according to claim 94 wherein the additional polypeptide comprises a *Chlamydia* polypeptide.

96. A pharmaceutical composition comprising a vaccine according to any one of claims 88 to 95 and a pharmaceutically acceptable carrier.

25 97. A pharmaceutical composition comprising an antibody according to claim 87 and a pharmaceutically acceptable carrier.



98. A method for preventing or treating *Chlamydia* infection comprising administering to a mammal an effective amount of the vaccine of any one of claims 73 to 81 and 88 to 95.

5 99. A method for preventing or treating *Chlamydia* infection comprising administering to a mammal an effective amount of the composition of any one of claims 82, 96 and 97.

100. A method for preventing or treating *Chlamydia* infection comprising administering to a mammal an effective  
10 amount of the fusion protein of any one of claims 83 to 86.

101. A method for preventing or treating *Chlamydia* infection comprising administering to a mammal an effective amount of the antibody of claim 87.

102. A commercial package comprising at least one nucleic  
15 acid selected from any one of:

(i) SEQ ID No: 5;

(ii) a nucleic acid sequence which encodes a polypeptide encoded by SEQ ID No: 5;

(iii) a nucleic acid sequence which encodes a  
20 polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by SEQ ID No: 5; and

(iv) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in SEQ ID No: 6;

(v) a nucleic acid sequence as defined in (i), (ii)  
25 or (iv), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iv);

wherein each first nucleic acid is capable of being expressed; and

instructions for use in eliciting an immunoprotective response in a mammal.

5 103. A commercial package comprising at least one nucleic acid selected from any one of:

(i) a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 5;

(ii) a nucleic acid sequence which encodes an  
10 immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 6;

(iii) a nucleic acid sequence as defined in (i) or (ii), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is  
15 at least 75% identical in amino acid sequence to the corresponding fragment of (i) or (ii);

wherein each first nucleic acid is capable of being expressed; and

instructions for use in eliciting an immunoprotective  
20 response in a mammal.

104. A commercial package comprising at least one polypeptide selected from any one of:

(i) a polypeptide encoded by SEQ ID NO: 5;

(ii) a polypeptide which is at least 75% identical in  
25 amino acid sequence to SEQ ID NO: 6 or to the polypeptide encoded by SEQ ID NO: 5;

(iii) a polypeptide of SEQ ID NO: 6; and

(iv) a polypeptide as defined in (i), (ii) or (iii) which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i),  
5 (ii) or (iii); and

instructions for use in eliciting an immunoprotective response in a mammal.

105. A commercial package comprising at least one polypeptide selected from any one of:

10 (i) a polypeptide encoded by a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO:  
5;

(ii) a polypeptide which is an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No:  
15 6;

(iii) a polypeptide as defined in (i) or (ii), which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) or (ii); and

20 instructions for use in eliciting an immunoprotective response in a mammal.

106. Expression plasmid pCACPNM208 as shown in Figure 23.

107. A vaccine comprising a vaccine vector and at least one first nucleic acid selected from:

25 (i) a nucleic acid encoding a polypeptide of any one of SEQ ID Nos: 44 to 47; and

(ii) a nucleic acid sequence as defined in (i) which has been modified to encode a modified conservatively

substituted polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i).

- 5 108. A vaccine comprising a vaccine vector and at least one first polypeptide selected from:

(i) a polypeptide of any one of SEQ ID Nos: 44 to 47;  
and

- (ii) a polypeptide as defined in (i) which has been  
10 modified by conservative substitution, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i).

109. A vaccine comprising a vaccine vector and at least  
15 one first nucleic acid selected from any one of:

(i) SEQ ID No: 7;

(ii) a nucleic acid sequence which encodes a polypeptide encoded by SEQ ID No: 7;

- (iii) a nucleic acid sequence which encodes a  
20 polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by SEQ ID No: 7; and

(iv) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in SEQ ID No: 8;

- (v) a nucleic acid sequence as defined in (i), (ii)  
25 or (iv), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iv);

wherein each first nucleic acid is capable of being expressed.

110. A vaccine comprising a vaccine vector and at least one first nucleic acid selected from any one of:

5 (i) a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 7;

(ii) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 8;

10 (iii) a nucleic acid sequence as defined in (i) or (ii), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding fragment of (i) or (ii);

15 wherein each first nucleic acid is capable of being expressed.

111. A vaccine comprising a vaccine vector and at least one first nucleic acid encoding a fusion protein, wherein the fusion protein comprises:

20 (a) a first polypeptide encoded by a nucleic acid selected from any one of:

(i) SEQ ID No: 7;

(ii) a nucleic acid sequence which encodes a polypeptide encoded by SEQ ID No: 7;

25 (iii) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by SEQ ID No: 7; and

(iv) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in SEQ ID No: 8;

(v) a nucleic acid sequence as defined in (i), (ii) or (iv), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iv); and

(b) a second polypeptide;

wherein each first nucleic acid is capable of being expressed.

112. A vaccine comprising a vaccine vector and at least one first nucleic acid encoding a fusion protein, wherein the fusion protein comprises:

(a) a first polypeptide encoded by a nucleic acid selected from any one of:

(i) a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 7;

(ii) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 8;

(iii) a nucleic acid sequence as defined in (i) or (ii), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding fragment of (i) or (ii); and

(b) a second polypeptide;

wherein each first nucleic acid is capable of being expressed.

113. The vaccine of claim 111 or 112 wherein the second polypeptide is a heterologous signal peptide.

5 114. The vaccine of claim 111 or 112 wherein the second polypeptide has adjuvant activity.

115. The vaccine of any one of claims 109 to 114 wherein wherein each first nucleic acid is operatively linked to one or more expression control sequences.

10 116. A vaccine according to any one of claims 109 to 115, further comprising a second nucleic acid encoding an additional polypeptide which enhances the immune response to the polypeptide expressed by the first nucleic acid.

117. The vaccine of claim 116 wherein the second nucleic  
15 acid encodes an additional *Chlamydia* polypeptide.

118. A pharmaceutical composition comprising a vaccine according to any one of claims 109 to 117 and a pharmaceutically acceptable carrier.

119. A fusion protein comprising a first and a second  
20 polypeptide, wherein the first polypeptide is selected from any one of:

(i) a polypeptide encoded by SEQ ID NO: 7;

(ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 8 or to the polypeptide  
25 encoded by SEQ ID NO: 7;

(iii) a polypeptide of SEQ ID NO: 8; and

(iv) a polypeptide as defined in (i), (ii) or (iii) which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i),  
5 (ii) or (iii).

120. A fusion protein comprising a first and a second polypeptide, wherein the first polypeptide is selected from any one of:

(i) a polypeptide encoded by a nucleic acid sequence  
10 comprising at least 36 consecutive nucleotides from SEQ ID NO: 7;

(ii) a polypeptide which is an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 8;

15 (iii) a polypeptide as defined in (i) or (ii), which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) or (ii).

121. The fusion protein of claim 119 or 120 wherein the  
20 second polypeptide is a heterologous signal peptide.

122. The fusion protein of claim 119 or 120 wherein the second polypeptide has adjuvant activity.

123. An antibody against the fusion protein of any one of claims 119 to 121.

25 124. A vaccine comprising at least one first polypeptide selected from any one of:

(i) a polypeptide encoded by SEQ ID NO: 7;



(ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 8 or to the polypeptide encoded by SEQ ID NO: 7;

(iii) a polypeptide of SEQ ID NO: 8; and

5 (iv) a polypeptide as defined in (i), (ii) or (iii) which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iii).

10 125. A vaccine comprising at least one first polypeptide selected from any one of:

(i) a polypeptide encoded by a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 7;

15 (ii) a polypeptide which is an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 8;

(iii) a polypeptide as defined in (i) or (ii), which has been modified without loss of immunogenicity and is at  
20 least 75% identical in amino acid sequence to the corresponding polypeptide of (i) or (ii).

126. A vaccine comprising at least one fusion protein, wherein the fusion protein comprises a first and a second polypeptide, wherein the first polypeptide is selected from any  
25 one of:

(i) a polypeptide encoded by SEQ ID NO: 7;

(ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 8 or to the polypeptide encoded by SEQ ID NO: 7;

(iii) a polypeptide of SEQ ID NO: 8; and

(iv) a polypeptide as defined in (i), (ii) or (iii) which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the  
5 corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iii).

127. A vaccine comprising at least one fusion protein, wherein the fusion protein comprises a first and a second polypeptide, wherein the first polypeptide is selected from any  
10 one of:

(i) a polypeptide encoded by a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 7;

(ii) a polypeptide which is an immunogenic fragment  
15 comprising at least 12 consecutive amino acids from SEQ ID No: 8;

(iii) a polypeptide as defined in (i) or (ii), which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding  
20 polypeptide of (i) or (ii).

128. The vaccine of claim 126 or 127 wherein the second polypeptide is a heterologous signal peptide.

129. The vaccine of claim 126 or 127 wherein the second polypeptide has adjuvant activity.

25 130. A vaccine according to any one of claims 124 to 129, further comprising an additional polypeptide which enhances the immune response to the first polypeptide.

131. The vaccine according to claim 130 wherein the additional polypeptide comprises a *Chlamydia* polypeptide.

132. A pharmaceutical composition comprising a vaccine according to any one of claims 124 to 131 and a pharmaceutically acceptable carrier.

133. A pharmaceutical composition comprising an antibody  
5 according to claim 123 and a pharmaceutically acceptable carrier.

134. A method for preventing or treating *Chlamydia* infection comprising administering to a mammal an effective amount of the vaccine of any one of claims 109 to 117 and 124  
10 to 131.

135. A method for preventing or treating *Chlamydia* infection comprising administering to a mammal an effective amount of the composition of any one of claims 118, 132 and 133.

15 136. A method for preventing or treating *Chlamydia* infection comprising administering to a mammal an effective amount of the fusion protein of any one of claims 119 to 122.

137. A method for preventing or treating *Chlamydia* infection comprising administering to a mammal an effective  
20 amount of the antibody of claim 123.

138. A commercial package comprising at least one nucleic acid selected from any one of:

(i) SEQ ID No: 7;

(ii) a nucleic acid sequence which encodes a  
25 polypeptide encoded by SEQ ID No: 7;

(iii) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by SEQ ID No: 7; and

(iv) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in SEQ ID No: 8;

(v) a nucleic acid sequence as defined in (i), (ii) or (iv), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iv);

wherein each first nucleic acid is capable of being expressed; and

instructions for use in eliciting an immunoprotective response in a mammal.

139. A commercial package comprising at least one nucleic acid selected from any one of:

(i) a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 7;

(ii) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 8;

(iii) a nucleic acid sequence as defined in (i) or (ii), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding fragment of (i) or (ii);

wherein each first nucleic acid is capable of being expressed; and

instructions for use in eliciting an immunoprotective response in a mammal.

140. A commercial package comprising at least one polypeptide selected from any one of:

(i) a polypeptide encoded by SEQ ID NO: 7;

(ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 8 or to the polypeptide encoded by SEQ ID NO: 7;

(iii) a polypeptide of SEQ ID NO: 8; and

(iv) a polypeptide as defined in (i), (ii) or (iii) which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iii); and

instructions for use in eliciting an immunoprotective response in a mammal.

141. A commercial package comprising at least one polypeptide selected from any one of:

(i) a polypeptide encoded by a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 7;

(ii) a polypeptide which is an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 8;

(iii) a polypeptide as defined in (i) or (ii), which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) or (ii);

and instructions for use in eliciting an immunoprotective response in a mammal.

142. Expression plasmid pCACPNM1096 as shown in Figure 24.

143. A vaccine comprising a vaccine vector and at least one first nucleic acid selected from:

(i) a nucleic acid encoding a polypeptide of any one  
5 of SEQ ID Nos: 48 to 51; and

(ii) a nucleic acid sequence as defined in (i) which has been modified to encode a modified conservatively substituted polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino  
10 acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i).

144. A vaccine comprising a vaccine vector and at least one first polypeptide selected from:

(i) a polypeptide of any one of SEQ ID Nos: 48 to 51;  
15 and

(ii) a polypeptide as defined in (i) which has been modified by conservative substitution, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding  
20 polypeptide encoded by the nucleic acid of (i).

145. A vaccine comprising a vaccine vector and at least one first nucleic acid selected from any one of:

(i) SEQ ID No: 9;

(ii) a nucleic acid sequence which encodes a  
25 polypeptide encoded by SEQ ID No: 9;

(iii) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by SEQ ID No: 9; and

(iv) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in SEQ ID No: 10;

(v) a nucleic acid sequence as defined in (i), (ii) or (iv), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iv);

wherein each first nucleic acid is capable of being expressed.

146. A vaccine comprising a vaccine vector and at least one first nucleic acid selected from any one of:

(i) a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 9;

(ii) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 10;

(iii) a nucleic acid sequence as defined in (i) or (ii), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding fragment of (i) or (ii);

wherein each first nucleic acid is capable of being expressed.

147. A vaccine comprising a vaccine vector and at least one first nucleic acid encoding a fusion protein, wherein the fusion protein comprises:

(a) a first polypeptide encoded by a nucleic acid selected from any one of:

(i) SEQ ID No: 9;

(ii) a nucleic acid sequence which encodes a polypeptide encoded by SEQ ID No: 9;

(iii) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by SEQ ID No: 9; and

(iv) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in SEQ ID No: 10;

(v) a nucleic acid sequence as defined in (i), (ii) or (iv), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iv); and

(b) a second polypeptide;

wherein each first nucleic acid is capable of being expressed.

148. A vaccine comprising a vaccine vector and at least one first nucleic acid encoding a fusion protein, wherein the fusion protein comprises:

(a) a first polypeptide encoded by a nucleic acid selected from any one of:

(i) a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 9;

(ii) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 10;



(iii) a nucleic acid sequence as defined in (i) or (ii), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the  
5 corresponding fragment of (i) or (ii); and

(b) a second polypeptide;

wherein each first nucleic acid is capable of being expressed.

149. The vaccine of claim 147 or 148 wherein the second  
10 polypeptide is a heterologous signal peptide.

150. The vaccine of claim 147 or 148 wherein the second polypeptide has adjuvant activity.

151. The vaccine of any one of claims 145 to 150 wherein each first nucleic acid is operatively linked to one or more  
15 expression control sequences.

152. A vaccine according to any one of claims 145 to 151, further comprising a second nucleic acid encoding an additional polypeptide which enhances the immune response to the polypeptide expressed by the first nucleic acid.

20 153. The vaccine of claim 152 wherein the second nucleic acid encodes an additional *Chlamydia* polypeptide.

154. A pharmaceutical composition comprising a vaccine according to any one of claims 145 to 153 and a pharmaceutically acceptable carrier.

25 155. A fusion protein comprising a first and a second polypeptide, wherein the first polypeptide is selected from any one of:

(i) a polypeptide encoded by SEQ ID NO: 9;

(ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 10 or to the polypeptide encoded by SEQ ID NO: 9;

(iii) a polypeptide of SEQ ID NO: 10; and

5 (iv) a polypeptide as defined in (i), (ii) or (iii) which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iii).

10 156. A fusion protein comprising a first and a second polypeptide, wherein the first polypeptide is selected from any one of:

(i) a polypeptide encoded by a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO:  
15 9;

(ii) a polypeptide which is an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 10;

(iii) a polypeptide as defined in (i) or (ii), which  
20 has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) or (ii).

157. The fusion protein of claim 155 or 156 wherein the second polypeptide is a heterologous signal peptide.

25 158. The fusion protein of claim 155 or 156 wherein the second polypeptide has adjuvant activity.

159. An antibody against the fusion protein of any one of claims 155 to 157.

160. A vaccine comprising at least one first polypeptide selected from any one of:

(i) a polypeptide encoded by SEQ ID NO: 9;

(ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 10 or to the polypeptide encoded by SEQ ID NO: 9;

(iii) a polypeptide of SEQ ID NO: 10; and

(iv) a polypeptide as defined in (i), (ii) or (iii) which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iii).

161. A vaccine comprising at least one first polypeptide selected from any one of:

(i) a polypeptide encoded by a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 9;

(ii) a polypeptide which is an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 10;

(iii) a polypeptide as defined in (i) or (ii), which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) or (ii).

162. A vaccine comprising at least one fusion protein, wherein the fusion protein comprises a first and a second polypeptide, wherein the first polypeptide is selected from any one of:

(i) a polypeptide encoded by SEQ ID NO: 9;

(ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 10 or to the polypeptide encoded by SEQ ID NO: 9;

5 (iii) a polypeptide of SEQ ID NO: 10; and

(iv) a polypeptide as defined in (i), (ii) or (iii) which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i),  
10 (ii) or (iii).

163. A vaccine comprising at least one fusion protein, wherein the fusion protein comprises a first and a second polypeptide, wherein the first polypeptide is selected from any one of:

15 (i) a polypeptide encoded by a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 9;

(ii) a polypeptide which is an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No:  
20 10;

(iii) a polypeptide as defined in (i) or (ii), which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) or (ii).

25 164. The vaccine of claim 162 or 163 wherein the second polypeptide is a heterologous signal peptide.

165. The vaccine of claim 162 or 163 wherein the second polypeptide has adjuvant activity.

166. A vaccine according to any one of claims 160 to 165, further comprising an additional polypeptide which enhances the immune response to the first polypeptide.

167. The vaccine according to claim 166 wherein the  
5 additional polypeptide comprises a *Chlamydia* polypeptide.

168. A pharmaceutical composition comprising a vaccine according to any one of claims 160 to 167 and a pharmaceutically acceptable carrier.

169. A pharmaceutical composition comprising an antibody  
10 according to claim 159 and a pharmaceutically acceptable carrier.

170. A method for preventing or treating *Chlamydia* infection comprising administering to a mammal an effective amount of the vaccine of any one of claims 145 to 153 and 160  
15 to 167.

171. A method for preventing or treating *Chlamydia* infection comprising administering to a mammal an effective amount of the composition of any one of claims 154, 168 and 169.

20 172. A method for preventing or treating *Chlamydia* infection comprising administering to a mammal an effective amount of the fusion protein of any one of claims 155 to 158.

173. A method for preventing or treating *Chlamydia* infection comprising administering to a mammal an effective  
25 amount of the antibody of claim 159.

174. A commercial package comprising at least one nucleic acid selected from any one of:

(i) SEQ ID No: 9;

(ii) a nucleic acid sequence which encodes a polypeptide encoded by SEQ ID No: 9;

(iii) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid  
5 sequence to the polypeptide encoded by SEQ ID No: 9; and

(iv) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in SEQ ID No: 10;

(v) a nucleic acid sequence as defined in (i), (ii) or (iv), which has been modified to encode a modified  
10 polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iv);

wherein each first nucleic acid is capable of being  
15 expressed; and

instructions for use in eliciting an immunoprotective response in a mammal.

175. A commercial package comprising at least one nucleic acid selected from any one of:

20 (i) a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 9;

(ii) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 10;

25 (iii) a nucleic acid sequence as defined in (i) or (ii), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding fragment of (i) or (ii);

wherein each first nucleic acid is capable of being expressed; and

instructions for use in eliciting an immunoprotective response in a mammal.

5 176. A commercial package comprising at least one polypeptide selected from any one of:

(i) a polypeptide encoded by SEQ ID NO: 9;

(ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 10 or to the polypeptide  
10 encoded by SEQ ID NO: 9;

(iii) a polypeptide of SEQ ID NO: 10; and

(iv) a polypeptide as defined in (i), (ii) or (iii) which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the  
15 corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iii); and

instructions for use in eliciting an immunoprotective response in a mammal.

177. A commercial package comprising at least one  
20 polypeptide selected from any one of:

(i) a polypeptide encoded by a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 9;

(ii) a polypeptide which is an immunogenic fragment  
25 comprising at least 12 consecutive amino acids from SEQ ID No: 10;

(iii) a polypeptide as defined in (i) or (ii), which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) or (ii); and

5 instructions for use in eliciting an immunoprotective response in a mammal.

178. Expression plasmid pCACPNM1097 as shown in Figure 25.

179. A vaccine comprising a vaccine vector and at least one first nucleic acid selected from:

10 (i) a nucleic acid encoding a polypeptide of any one of SEQ ID Nos: 52 to 56; and

(ii) a nucleic acid sequence as defined in (i) which has been modified to encode a modified conservatively substituted polypeptide, wherein the modified polypeptide  
15 retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i).

180. A vaccine comprising a vaccine vector and at least one first polypeptide selected from:

20 (i) a polypeptide of any one of SEQ ID Nos: 52 to 56; and

(ii) a polypeptide as defined in (i) which has been modified by conservative substitution, wherein the modified polypeptide retains immunogenicity and is at least 75%  
25 identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i).

181. A vaccine comprising a vaccine vector and at least one first nucleic acid selected from any one of:



(i) SEQ ID No: 11;

(ii) a nucleic acid sequence which encodes a polypeptide encoded by SEQ ID No: 11;

(iii) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by SEQ ID No: 11; and

(iv) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in SEQ ID No: 12;

(v) a nucleic acid sequence as defined in (i), (ii) or (iv), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iv);

wherein each first nucleic acid is capable of being expressed.

182. A vaccine comprising a vaccine vector and at least one first nucleic acid selected from any one of:

(i) a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 11;

(ii) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 12;

(iii) a nucleic acid sequence as defined in (i) or (ii), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding fragment of (i) or (ii);

wherein each first nucleic acid is capable of being expressed.

183. A vaccine comprising a vaccine vector and at least one first nucleic acid encoding a fusion protein, wherein the fusion protein comprises:

(a) a first polypeptide encoded by a nucleic acid selected from any one of:

(i) SEQ ID No: 11;

(ii) a nucleic acid sequence which encodes a polypeptide encoded by SEQ ID No: 11;

(iii) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by SEQ ID No: 11; and

(iv) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in SEQ ID No: 12;

(v) a nucleic acid sequence as defined in (i), (ii) or (iv), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iv); and

(b) a second polypeptide;

wherein each first nucleic acid is capable of being expressed.

184. A vaccine comprising a vaccine vector and at least one first nucleic acid encoding a fusion protein, wherein the fusion protein comprises:

(a) a first polypeptide encoded by a nucleic acid selected from any one of:

(i) a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 11;

5 (ii) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 12;

(iii) a nucleic acid sequence as defined in (i) or (ii), which has been modified to encode a modified polypeptide,  
10 wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding fragment of (i) or (ii); and

(b) a second polypeptide;

wherein each first nucleic acid is capable of being  
15 expressed.

185. The vaccine of claim 183 or 184 wherein the second polypeptide is a heterologous signal peptide.

186. The vaccine of claim 183 or 184 wherein the second polypeptide has adjuvant activity.

20 187. The vaccine of any one of claims 181 to 186 wherein wherein each first nucleic acid is operatively linked to one or more expression control sequences.

188. A vaccine according to any one of claims 181 to 187, further comprising a second nucleic acid encoding an additional  
25 polypeptide which enhances the immune response to the polypeptide expressed by the first nucleic acid.

189. The vaccine of claim 188 wherein the second nucleic acid encodes an additional *Chlamydia* polypeptide.

190. A pharmaceutical composition comprising a vaccine according to any one of claims 181 to 189 and a pharmaceutically acceptable carrier.

191. A fusion protein comprising a first and a second polypeptide, wherein the first polypeptide is selected from any one of:

(i) a polypeptide encoded by SEQ ID NO: 11;

(ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 12 or to the polypeptide encoded by SEQ ID NO: 11;

(iii) a polypeptide of SEQ ID NO: 12; and

(iv) a polypeptide as defined in (i), (ii) or (iii) which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iii).

192. A fusion protein comprising a first and a second polypeptide, wherein the first polypeptide is selected from any one of:

(i) a polypeptide encoded by a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 11;

(ii) a polypeptide which is an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 12;

(iii) a polypeptide as defined in (i) or (ii), which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) or (ii).

193. The fusion protein of claim 191 or 192 wherein the second polypeptide is a heterologous signal peptide.

194. The fusion protein of claim 191 or 192 wherein the second polypeptide has adjuvant activity.

5 195. An antibody against the fusion protein of any one of claims 191 to 193.

196. A vaccine comprising at least one first polypeptide selected from any one of:

(i) a polypeptide encoded by SEQ ID NO: 11;

10 (ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 12 or to the polypeptide encoded by SEQ ID NO: 11;

(iii) a polypeptide of SEQ ID NO: 12; and

(iv) a polypeptide as defined in (i), (ii) or (iii)  
15 which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iii).

197. A vaccine comprising at least one first polypeptide  
20 selected from any one of:

(i) a polypeptide encoded by a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 11;

(ii) a polypeptide which is an immunogenic fragment  
25 comprising at least 12 consecutive amino acids from SEQ ID No: 12;

(iii) a polypeptide as defined in (i) or (ii), which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) or (ii).

5 198. A vaccine comprising at least one fusion protein, wherein the fusion protein comprises a first and a second polypeptide, wherein the first polypeptide is selected from any one of:

(i) a polypeptide encoded by SEQ ID NO: 11;

10 (ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 12 or to the polypeptide encoded by SEQ ID NO: 11;

(iii) a polypeptide of SEQ ID NO: 12; and

(iv) a polypeptide as defined in (i), (ii) or (iii)  
15 which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iii).

199. A vaccine comprising at least one fusion protein,  
20 wherein the fusion protein comprises a first and a second polypeptide, wherein the first polypeptide is selected from any one of:

(i) a polypeptide encoded by a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO:  
25 11;

(ii) a polypeptide which is an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 12;

(iii) a polypeptide as defined in (i) or (ii), which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) or (ii).

5 200. The vaccine of claim 198 or 199 wherein the second polypeptide is a heterologous signal peptide.

201. The vaccine of claim 198 or 199 wherein the second polypeptide has adjuvant activity.

202. A vaccine according to any one of claims 196 to 201,  
10 further comprising an additional polypeptide which enhances the immune response to the first polypeptide.

203. The vaccine according to claim 202 wherein the additional polypeptide comprises a *Chlamydia* polypeptide.

204. A pharmaceutical composition comprising a vaccine  
15 according to any one of claims 196 to 203 and a pharmaceutically acceptable carrier.

205. A pharmaceutical composition comprising an antibody according to claim 195 and a pharmaceutically acceptable carrier.

20 206. A method for preventing or treating *Chlamydia* infection comprising administering to a mammal an effective amount of the vaccine of any one of claims 181 to 189 and 196 to 203.

207. A method for preventing or treating *Chlamydia*  
25 infection comprising administering to a mammal an effective amount of the composition of any one of claims 190, 204 and 205.

208. A method for preventing or treating *Chlamydia* infection comprising administering to a mammal an effective amount of the fusion protein of any one of claims 191 to 194.

209. A method for preventing or treating *Chlamydia*  
5 infection comprising administering to a mammal an effective amount of the antibody of claim 195.

210. A commercial package comprising at least one nucleic acid selected from any one of:

(i) SEQ ID No: 11;

10 (ii) a nucleic acid sequence which encodes a polypeptide encoded by SEQ ID No: 11;

(iii) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by SEQ ID No: 11; and

15 (iv) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in SEQ ID No: 12;

(v) a nucleic acid sequence as defined in (i), (ii) or (iv), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains  
20 immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iv);

wherein each first nucleic acid is capable of being expressed; and

25 instructions for use in eliciting an immunoprotective response in a mammal.

211. A commercial package comprising at least one nucleic acid selected from any one of:



(i) a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 11;

(ii) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 12;

(iii) a nucleic acid sequence as defined in (i) or (ii), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding fragment of (i) or (ii);

wherein each first nucleic acid is capable of being expressed; and

instructions for use in eliciting an immunoprotective response in a mammal.

212. A commercial package comprising at least one polypeptide selected from any one of:

(i) a polypeptide encoded by SEQ ID NO: 11;

(ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 12 or to the polypeptide encoded by SEQ ID NO: 11;

(iii) a polypeptide of SEQ ID NO: 12; and

(iv) a polypeptide as defined in (i), (ii) or (iii) which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iii); and

instructions for use in eliciting an immunoprotective response in a mammal.

213. A commercial package comprising at least one polypeptide selected from any one of:

(i) a polypeptide encoded by a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO:  
5 11;

(ii) a polypeptide which is an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No:  
12;

(iii) a polypeptide as defined in (i) or (ii), which  
10 has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) or (ii); and

instructions for use in eliciting an immunoprotective response in a mammal.

15 214. Expression plasmid pCACPNM908 as shown in Figure 26.

215. A vaccine comprising a vaccine vector and at least one first nucleic acid selected from:

(i) a nucleic acid encoding a polypeptide of any one of SEQ ID Nos: 57 to 60; and

20 (ii) a nucleic acid sequence as defined in (i) which has been modified to encode a modified conservatively substituted polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the  
25 nucleic acid of (i).

216. A vaccine comprising a vaccine vector and at least one first polypeptide selected from:

(i) a polypeptide of any one of SEQ ID Nos: 57 to 60;  
and

(ii) a polypeptide as defined in (i) which has been modified by conservative substitution, wherein the modified  
5 polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i).

217. A vaccine comprising a vaccine vector and at least one first nucleic acid selected from any one of:

10 (i) SEQ ID No: 13;

(ii) a nucleic acid sequence which encodes a polypeptide encoded by SEQ ID No: 13;

(iii) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid  
15 sequence to the polypeptide encoded by SEQ ID No: 13; and

(iv) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in SEQ ID No: 14;

(v) a nucleic acid sequence as defined in (i), (ii) or (iv), which has been modified to encode a modified  
20 polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iv);

wherein each first nucleic acid is capable of being  
25 expressed.

218. A vaccine comprising a vaccine vector and at least one first nucleic acid selected from any one of:

(i) a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 13;

(ii) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 14;

(iii) a nucleic acid sequence as defined in (i) or (ii), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding fragment of (i) or (ii);

wherein each first nucleic acid is capable of being expressed.

219. A vaccine comprising a vaccine vector and at least one first nucleic acid encoding a fusion protein, wherein the fusion protein comprises:

(a) a first polypeptide encoded by a nucleic acid selected from any one of:

(i) SEQ ID No: 13;

(ii) a nucleic acid sequence which encodes a polypeptide encoded by SEQ ID No: 13;

(iii) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by SEQ ID No: 13; and

(iv) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in SEQ ID No: 14;

(v) a nucleic acid sequence as defined in (i), (ii) or (iv), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains

immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iv); and

(b) a second polypeptide;

5 wherein each first nucleic acid is capable of being expressed.

220. A vaccine comprising a vaccine vector and at least one first nucleic acid encoding a fusion protein, wherein the fusion protein comprises:

(a) a first polypeptide encoded by a nucleic acid  
10 selected from any one of:

(i) a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 13;

(ii) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino  
15 acids from SEQ ID No: 14;

(iii) a nucleic acid sequence as defined in (i) or (ii), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the  
20 corresponding fragment of (i) or (ii); and

(b) a second polypeptide;

wherein each first nucleic acid is capable of being expressed.

221. The vaccine of claim 219 or 220 wherein the second  
25 polypeptide is a heterologous signal peptide.

222. The vaccine of claim 219 or 220 wherein the second polypeptide has adjuvant activity.

223. The vaccine of any one of claims 217 to 222 wherein wherein each first nucleic acid is operatively linked to one or more expression control sequences.

224. A vaccine according to any one of claims 217 to 223,  
5 further comprising a second nucleic acid encoding an additional polypeptide which enhances the immune response to the polypeptide expressed by the first nucleic acid.

225. The vaccine of claim 224 wherein the second nucleic acid encodes an additional *Chlamydia* polypeptide.

10 226. A pharmaceutical composition comprising a vaccine according to any one of claims 217 to 225 and a pharmaceutically acceptable carrier.

227. A fusion protein comprising a first and a second polypeptide, wherein the first polypeptide is selected from any  
15 one of:

(i) a polypeptide encoded by SEQ ID NO: 13;

(ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 14 or to the polypeptide encoded by SEQ ID NO: 13;

20 (iii) a polypeptide of SEQ ID NO: 14; and

(iv) a polypeptide as defined in (i), (ii) or (iii) which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i),  
25 (ii) or (iii).

228. A fusion protein comprising a first and a second polypeptide, wherein the first polypeptide is selected from any one of:

(i) a polypeptide encoded by a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 13;

(ii) a polypeptide which is an immunogenic fragment  
5 comprising at least 12 consecutive amino acids from SEQ ID No: 14;

(iii) a polypeptide as defined in (i) or (ii), which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding  
10 polypeptide of (i) or (ii).

229. The fusion protein of claim 227 or 228 wherein the second polypeptide is a heterologous signal peptide.

230. The fusion protein of claim 227 or 228 wherein the second polypeptide has adjuvant activity.

15 231. An antibody against the fusion protein of any one of claims 227 to 229.

232. A vaccine comprising at least one first polypeptide selected from any one of:

(i) a polypeptide encoded by SEQ ID NO: 13;

20 (ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 14 or to the polypeptide encoded by SEQ ID NO: 13;

(iii) a polypeptide of SEQ ID NO: 14; and

(iv) a polypeptide as defined in (i), (ii) or (iii)  
25 which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iii).

233. A vaccine comprising at least one first polypeptide selected from any one of:

(i) a polypeptide encoded by a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO:

5 13;

(ii) a polypeptide which is an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 14;

(iii) a polypeptide as defined in (i) or (ii), which  
10 has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) or (ii).

234. A vaccine comprising at least one fusion protein, wherein the fusion protein comprises a first and a second  
15 polypeptide, wherein the first polypeptide is selected from any one of:

(i) a polypeptide encoded by SEQ ID NO: 13;

(ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 14 or to the polypeptide  
20 encoded by SEQ ID NO: 13;

(iii) a polypeptide of SEQ ID NO: 14; and

(iv) a polypeptide as defined in (i), (ii) or (iii) which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the  
25 corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iii).

235. A vaccine comprising at least one fusion protein, wherein the fusion protein comprises a first and a second



polypeptide, wherein the first polypeptide is selected from any one of:

(i) a polypeptide encoded by a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO:

5 13;

(ii) a polypeptide which is an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 14;

(iii) a polypeptide as defined in (i) or (ii), which  
10 has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) or (ii).

236. The vaccine of claim 234 or 235 wherein the second polypeptide is a heterologous signal peptide.

15 237. The vaccine of claim 234 or 235 wherein the second polypeptide has adjuvant activity.

238. A vaccine according to any one of claims 232 to 237, further comprising an additional polypeptide which enhances the immune response to the first polypeptide.

20 239. The vaccine according to claim 238 wherein the additional polypeptide comprises a *Chlamydia* polypeptide.

240. A pharmaceutical composition comprising a vaccine according to any one of claims 232 to 239 and a pharmaceutically acceptable carrier.

25 241. A pharmaceutical composition comprising an antibody according to claim 231 and a pharmaceutically acceptable carrier.

242. A method for preventing or treating *Chlamydia* infection comprising administering to a mammal an effective amount of the vaccine of any one of claims 217 to 225 and 232 to 239.
- 5 243. A method for preventing or treating *Chlamydia* infection comprising administering to a mammal an effective amount of the composition of any one of claims 226, 240 and 241.
244. A method for preventing or treating *Chlamydia*  
10 infection comprising administering to a mammal an effective amount of the fusion protein of any one of claims 227 to 230.
245. A method for preventing or treating *Chlamydia* infection comprising administering to a mammal an effective amount of the antibody of claim 231.
- 15 246. A commercial package comprising at least one nucleic acid selected from any one of:
- (i) SEQ ID No: 13;
  - (ii) a nucleic acid sequence which encodes a polypeptide encoded by SEQ ID No: 13;
  - 20 (iii) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by SEQ ID No: 13; and
  - (iv) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in SEQ ID No: 14;
  - 25 (v) a nucleic acid sequence as defined in (i), (ii) or (iv), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid

sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iv);

wherein each first nucleic acid is capable of being expressed; and

5 instructions for use in eliciting an immunoprotective response in a mammal.

247. A commercial package comprising at least one nucleic acid selected from any one of:

(i) a nucleic acid sequence comprising at least 36  
10 consecutive nucleotides from SEQ ID NO: 13;

(ii) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 14;

(iii) a nucleic acid sequence as defined in (i) or  
15 (ii), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding fragment of (i) or (ii);

wherein each first nucleic acid is capable of being  
20 expressed; and

instructions for use in eliciting an immunoprotective response in a mammal.

248. A commercial package comprising at least one polypeptide selected from any one of:

25 (i) a polypeptide encoded by SEQ ID NO: 13;

(ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 14 or to the polypeptide encoded by SEQ ID NO: 13;

(iii) a polypeptide of SEQ ID NO: 14; and

5 (iv) a polypeptide as defined in (i), (ii) or (iii) which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iii); and

10 instructions for use in eliciting an immunoprotective response in a mammal.

249. A commercial package comprising at least one polypeptide selected from any one of:

(i) a polypeptide encoded by a nucleic acid sequence  
15 comprising at least 36 consecutive nucleotides from SEQ ID NO: 13;

(ii) a polypeptide which is an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 14;

20 (iii) a polypeptide as defined in (i) or (ii), which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) or (ii); and

instructions for use in eliciting an immunoprotective  
25 response in a mammal.

250. Expression plasmid pCACPNM909 as shown in Figure 27.

251. A vaccine comprising a vaccine vector and at least one first nucleic acid selected from:

(i) a nucleic acid encoding a polypeptide of any one of SEQ ID Nos: 61 to 63; and

(ii) a nucleic acid sequence as defined in (i) which has been modified to encode a modified conservatively substituted polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i).

252. A vaccine comprising a vaccine vector and at least one first polypeptide selected from:

(i) a polypeptide of any one of SEQ ID Nos: 61 to 63; and

(ii) a polypeptide as defined in (i) which has been modified by conservative substitution, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i).

253. A vaccine comprising a vaccine vector and at least one first nucleic acid selected from any one of:

20 (i) SEQ ID No: 15;

(ii) a nucleic acid sequence which encodes a polypeptide encoded by SEQ ID No: 15;

(iii) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by SEQ ID No: 15; and

(iv) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in SEQ ID No: 16;

(v) a nucleic acid sequence as defined in (i), (ii) or (iv), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iv);

wherein each first nucleic acid is capable of being expressed.

254. A vaccine comprising a vaccine vector and at least one first nucleic acid selected from any one of:

(i) a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 15;

(ii) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 16;

(iii) a nucleic acid sequence as defined in (i) or (ii), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding fragment of (i) or (ii);

wherein each first nucleic acid is capable of being expressed.

255. A vaccine comprising a vaccine vector and at least one first nucleic acid encoding a fusion protein, wherein the fusion protein comprises:

(a) a first polypeptide encoded by a nucleic acid selected from any one of:

(i) SEQ ID No: 15;

(ii) a nucleic acid sequence which encodes a polypeptide encoded by SEQ ID No: 15;

(iii) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid  
5 sequence to the polypeptide encoded by SEQ ID No: 15; and

(iv) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in SEQ ID No: 16;

(v) a nucleic acid sequence as defined in (i), (ii) or (iv), which has been modified to encode a modified  
10 polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iv); and

(b) a second polypeptide;

15 wherein each first nucleic acid is capable of being expressed.

256. A vaccine comprising a vaccine vector and at least one first nucleic acid encoding a fusion protein, wherein the fusion protein comprises:

20 (a) a first polypeptide encoded by a nucleic acid selected from any one of:

(i) a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 15;

(ii) a nucleic acid sequence which encodes an  
25 immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 16;

(iii) a nucleic acid sequence as defined in (i) or (ii), which has been modified to encode a modified polypeptide,

wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding fragment of (i) or (ii); and

(b) a second polypeptide;

5                wherein each first nucleic acid is capable of being expressed.

257.           The vaccine of claim 255 or 256 wherein the second polypeptide is a heterologous signal peptide.

258.           The vaccine of claim 255 or 256 wherein the second  
10 polypeptide has adjuvant activity.

259.           The vaccine of any one of claims 253 to 258 wherein wherein each first nucleic acid is operatively linked to one or more expression control sequences.

260.           A vaccine according to any one of claims 253 to 259,  
15 further comprising a second nucleic acid encoding an additional polypeptide which enhances the immune response to the polypeptide expressed by the first nucleic acid.

261.           The vaccine of claim 260 wherein the second nucleic acid encodes an additional *Chlamydia* polypeptide.

20 262.           A pharmaceutical composition comprising a vaccine according to any one of claims 253 to 261 and a pharmaceutically acceptable carrier.

263.           A fusion protein comprising a first and a second polypeptide, wherein the first polypeptide is selected from any  
25 one of:

(i) a polypeptide encoded by SEQ ID NO: 15;



(ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 16 or to the polypeptide encoded by SEQ ID NO: 15;

(iii) a polypeptide of SEQ ID NO: 16; and

5 (iv) a polypeptide as defined in (i), (ii) or (iii) which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iii).

10 264. A fusion protein comprising a first and a second polypeptide, wherein the first polypeptide is selected from any one of:

(i) a polypeptide encoded by a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO:  
15 15;

(ii) a polypeptide which is an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 16;

(iii) a polypeptide as defined in (i) or (ii), which  
20 has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) or (ii).

265. The fusion protein of claim 263 or 264 wherein the second polypeptide is a heterologous signal peptide.

25 266. The fusion protein of claim 263 or 264 wherein the second polypeptide has adjuvant activity.

267. An antibody against the fusion protein of any one of claims 263 to 265.

268. A vaccine comprising at least one first polypeptide selected from any one of:

(i) a polypeptide encoded by SEQ ID NO: 15;

(ii) a polypeptide which is at least 75% identical in  
5 amino acid sequence to SEQ ID NO: 16 or to the polypeptide encoded by SEQ ID NO: 15;

(iii) a polypeptide of SEQ ID NO: 16; and

(iv) a polypeptide as defined in (i), (ii) or (iii) which has been modified without loss of immunogenicity and is  
10 at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iii).

269. A vaccine comprising at least one first polypeptide selected from any one of:

15 (i) a polypeptide encoded by a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 15;

(ii) a polypeptide which is an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No:  
20 16;

(iii) a polypeptide as defined in (i) or (ii), which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) or (ii).

25 270. A vaccine comprising at least one fusion protein, wherein the fusion protein comprises a first and a second polypeptide, wherein the first polypeptide is selected from any one of:

- (i) a polypeptide encoded by SEQ ID NO: 15;
- (ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 16 or to the polypeptide encoded by SEQ ID NO: 15;
- 5 (iii) a polypeptide of SEQ ID NO: 16; and
- (iv) a polypeptide as defined in (i), (ii) or (iii) which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i),
- 10 (ii) or (iii).

271. A vaccine comprising at least one fusion protein, wherein the fusion protein comprises a first and a second polypeptide, wherein the first polypeptide is selected from any one of:

- 15 (i) a polypeptide encoded by a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 15;
- (ii) a polypeptide which is an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No:
- 20 16;
- (iii) a polypeptide as defined in (i) or (ii), which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) or (ii).

25 272. The vaccine of claim 270 or 271 wherein the second polypeptide is a heterologous signal peptide.

273. The vaccine of claim 270 or 271 wherein the second polypeptide has adjuvant activity.

274. A vaccine according to any one of claims 268 to 273, further comprising an additional polypeptide which enhances the immune response to the first polypeptide.

275. The vaccine according to claim 274 wherein the  
5 additional polypeptide comprises a *Chlamydia* polypeptide.

276. A pharmaceutical composition comprising a vaccine according to any one of claims 268 to 275 and a pharmaceutically acceptable carrier.

277. A pharmaceutical composition comprising an antibody  
10 according to claim 267 and a pharmaceutically acceptable carrier.

278. A method for preventing or treating *Chlamydia* infection comprising administering to a mammal an effective amount of the vaccine of any one of claims 253 to 261 and 268  
15 to 275.

279. A method for preventing or treating *Chlamydia* infection comprising administering to a mammal an effective amount of the composition of any one of claims 262, 276 and 277.

20 280. A method for preventing or treating *Chlamydia* infection comprising administering to a mammal an effective amount of the fusion protein of any one of claims 263 to 266.

281. A method for preventing or treating *Chlamydia* infection comprising administering to a mammal an effective  
25 amount of the antibody of claim 267.

282. A commercial package comprising at least one nucleic acid selected from any one of:

(i) SEQ ID No: 15;

(ii) a nucleic acid sequence which encodes a polypeptide encoded by SEQ ID No: 15;

(iii) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid  
5 sequence to the polypeptide encoded by SEQ ID No: 15; and

(iv) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in SEQ ID No: 16;

(v) a nucleic acid sequence as defined in (i), (ii) or (iv), which has been modified to encode a modified  
10 polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iv);

wherein each first nucleic acid is capable of being  
15 expressed; and

instructions for use in eliciting an immunoprotective response in a mammal.

283. A commercial package comprising at least one nucleic acid selected from any one of:

20 (i) a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 15;

(ii) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 16;

25 (iii) a nucleic acid sequence as defined in (i) or (ii), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding fragment of (i) or (ii);

wherein each first nucleic acid is capable of being expressed; and

instructions for use in eliciting an immunoprotective response in a mammal.

5 284. A commercial package comprising at least one polypeptide selected from any one of:

(i) a polypeptide encoded by SEQ ID NO: 15;

(ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 16 or to the polypeptide  
10 encoded by SEQ ID NO: 15;

(iii) a polypeptide of SEQ ID NO: 16; and

(iv) a polypeptide as defined in (i), (ii) or (iii) which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the  
15 corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iii); and

instructions for use in eliciting an immunoprotective response in a mammal.

285. A commercial package comprising at least one  
20 polypeptide selected from any one of:

(i) a polypeptide encoded by a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 15;

(ii) a polypeptide which is an immunogenic fragment  
25 comprising at least 12 consecutive amino acids from SEQ ID No: 16;

(iii) a polypeptide as defined in (i) or (ii), which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) or (ii); and

5           instructions for use in eliciting an immunoprotective response in a mammal.

286.       Expression plasmid pCACPNM440 as shown in Figure 28.

287.       A vaccine comprising a vaccine vector and at least one first nucleic acid selected from:

10           (i) a nucleic acid encoding a polypeptide of any one of SEQ ID Nos: 64 to 67; and

            (ii) a nucleic acid sequence as defined in (i) which has been modified to encode a modified conservatively substituted polypeptide, wherein the modified polypeptide  
15 retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i).

288.       A vaccine comprising a vaccine vector and at least one first polypeptide selected from:

20           (i) a polypeptide of any one of SEQ ID Nos: 64 to 67; and

            (ii) a polypeptide as defined in (i) which has been modified by conservative substitution, wherein the modified polypeptide retains immunogenicity and is at least 75%  
25 identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i).

289.       A vaccine comprising a vaccine vector and at least one first nucleic acid selected from any one of:

170

(i) SEQ ID No: 17;

(ii) a nucleic acid sequence which encodes a polypeptide encoded by SEQ ID No: 17;

(iii) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by SEQ ID No: 17; and

(iv) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in SEQ ID No: 18;

(v) a nucleic acid sequence as defined in (i), (ii) or (iv), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iv);

wherein each first nucleic acid is capable of being expressed.

290. A vaccine comprising a vaccine vector and at least one first nucleic acid selected from any one of:

(i) a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 17;

(ii) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 18;

(iii) a nucleic acid sequence as defined in (i) or (ii), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding fragment of (i) or (ii);



wherein each first nucleic acid is capable of being expressed.

291. A vaccine comprising a vaccine vector and at least one first nucleic acid encoding a fusion protein, wherein the  
5 fusion protein comprises:

(a) a first polypeptide encoded by a nucleic acid selected from any one of:

(i) SEQ ID No: 17;

(ii) a nucleic acid sequence which encodes a  
10 polypeptide encoded by SEQ ID No: 17;

(iii) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by SEQ ID No: 17; and

(iv) a nucleic acid sequence which encodes a  
15 polypeptide whose sequence is set forth in SEQ ID No: 18;

(v) a nucleic acid sequence as defined in (i), (ii) or (iv), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid  
20 sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iv); and

(b) a second polypeptide;

wherein each first nucleic acid is capable of being expressed.

292. A vaccine comprising a vaccine vector and at least  
25 one first nucleic acid encoding a fusion protein, wherein the fusion protein comprises:

(a) a first polypeptide encoded by a nucleic acid selected from any one of:

(i) a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 17;

5 (ii) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 18;

(iii) a nucleic acid sequence as defined in (i) or (ii), which has been modified to encode a modified polypeptide,  
10 wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding fragment of (i) or (ii); and

(b) a second polypeptide;

wherein each first nucleic acid is capable of being  
15 expressed.

293. The vaccine of claim 291 or 292 wherein the second polypeptide is a heterologous signal peptide.

294. The vaccine of claim 291 or 292 wherein the second polypeptide has adjuvant activity.

20 295. The vaccine of any one of claims 289 to 294 wherein wherein each first nucleic acid is operatively linked to one or more expression control sequences.

296. A vaccine according to any one of claims 289 to 295, further comprising a second nucleic acid encoding an additional  
25 polypeptide which enhances the immune response to the polypeptide expressed by the first nucleic acid.

297. The vaccine of claim 296 wherein the second nucleic acid encodes an additional *Chlamydia* polypeptide.

298. A pharmaceutical composition comprising a vaccine according to any one of claims 289 to 297 and a pharmaceutically acceptable carrier.

299. A fusion protein comprising a first and a second  
5 polypeptide, wherein the first polypeptide is selected from any one of:

(i) a polypeptide encoded by SEQ ID NO: 17;

(ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 18 or to the polypeptide  
10 encoded by SEQ ID NO: 17;

(iii) a polypeptide of SEQ ID NO: 18; and

(iv) a polypeptide as defined in (i), (ii) or (iii) which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the  
15 corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iii).

300. A fusion protein comprising a first and a second polypeptide, wherein the first polypeptide is selected from any one of:

20 (i) a polypeptide encoded by a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 17;

(ii) a polypeptide which is an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No:  
25 18;

(iii) a polypeptide as defined in (i) or (ii), which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) or (ii).

301. The fusion protein of claim 299 or 300 wherein the second polypeptide is a heterologous signal peptide.

302. The fusion protein of claim 299 or 300 wherein the second polypeptide has adjuvant activity.

5 303. An antibody against the fusion protein of any one of claims 299 to 301.

304. A vaccine comprising at least one first polypeptide selected from any one of:

(i) a polypeptide encoded by SEQ ID NO: 17;

10 (ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 18 or to the polypeptide encoded by SEQ ID NO: 17;

(iii) a polypeptide of SEQ ID NO: 18; and

(iv) a polypeptide as defined in (i), (ii) or (iii) which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iii).

15 305. A vaccine comprising at least one first polypeptide selected from any one of:

(i) a polypeptide encoded by a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 17;

(ii) a polypeptide which is an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 18;

(iii) a polypeptide as defined in (i) or (ii), which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) or (ii).

5 306. A vaccine comprising at least one fusion protein, wherein the fusion protein comprises a first and a second polypeptide, wherein the first polypeptide is selected from any one of:

(i) a polypeptide encoded by SEQ ID NO: 17;

10 (ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 18 or to the polypeptide encoded by SEQ ID NO: 17;

(iii) a polypeptide of SEQ ID NO: 18; and

(iv) a polypeptide as defined in (i), (ii) or (iii)  
15 which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iii).

307. A vaccine comprising at least one fusion protein,  
20 wherein the fusion protein comprises a first and a second polypeptide, wherein the first polypeptide is selected from any one of:

(i) a polypeptide encoded by a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO:  
25 17;

(ii) a polypeptide which is an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 18;

(iii) a polypeptide as defined in (i) or (ii), which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) or (ii).

5 308. The vaccine of claim 306 or 307 wherein the second polypeptide is a heterologous signal peptide.

309. The vaccine of claim 306 or 307 wherein the second polypeptide has adjuvant activity.

310. A vaccine according to any one of claims 304 to 309,  
10 further comprising an additional polypeptide which enhances the immune response to the first polypeptide.

311. The vaccine according to claim 310 wherein the additional polypeptide comprises a *Chlamydia* polypeptide.

312. A pharmaceutical composition comprising a vaccine  
15 according to any one of claims 304 to 311 and a pharmaceutically acceptable carrier.

313. A pharmaceutical composition comprising an antibody according to claim 303 and a pharmaceutically acceptable carrier.

20 314. A method for preventing or treating *Chlamydia* infection comprising administering to a mammal an effective amount of the vaccine of any one of claims 289 to 297 and 304 to 311.

315. A method for preventing or treating *Chlamydia*  
25 infection comprising administering to a mammal an effective amount of the composition of any one of claims 298, 312 and 313.

316. A method for preventing or treating *Chlamydia* infection comprising administering to a mammal an effective amount of the fusion protein of any one of claims 299 to 302.

317. A method for preventing or treating *Chlamydia*  
5 infection comprising administering to a mammal an effective amount of the antibody of claim 303.

318. A commercial package comprising at least one nucleic acid selected from any one of:

(i) SEQ ID No: 17;

10 (ii) a nucleic acid sequence which encodes a polypeptide encoded by SEQ ID No: 17;

(iii) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by SEQ ID No: 17; and

15 (iv) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in SEQ ID No: 18;

(v) a nucleic acid sequence as defined in (i), (ii) or (iv), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains  
20 immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iv);

wherein each first nucleic acid is capable of being expressed; and

25 instructions for use in eliciting an immunoprotective response in a mammal.

319. A commercial package comprising at least one nucleic acid selected from any one of:

(i) a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 17;

(ii) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 18;

(iii) a nucleic acid sequence as defined in (i) or (ii), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding fragment of (i) or (ii);

wherein each first nucleic acid is capable of being expressed; and

instructions for use in eliciting an immunoprotective response in a mammal.

320. A commercial package comprising at least one polypeptide selected from any one of:

(i) a polypeptide encoded by SEQ ID NO: 17;

(ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 18 or to the polypeptide encoded by SEQ ID NO: 17;

(iii) a polypeptide of SEQ ID NO: 18; and

(iv) a polypeptide as defined in (i), (ii) or (iii) which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iii);

and instructions for use in eliciting an immunoprotective response in a mammal.



321. A commercial package comprising at least one polypeptide selected from any one of:

(i) a polypeptide encoded by a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO:  
5 17;

(ii) a polypeptide which is an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No:  
18;

(iii) a polypeptide as defined in (i) or (ii), which  
10 has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) or (ii);

and instructions for use in eliciting an immunoprotective response in a mammal.

15 322. Expression plasmid pCACPNM459 as shown in Figure 29.

323. A vaccine comprising a vaccine vector and at least one first nucleic acid selected from:

(i) a nucleic acid encoding a polypeptide of any one of SEQ ID Nos: 68 to 71; and

20 (ii) a nucleic acid sequence as defined in (i) which has been modified to encode a modified conservatively substituted polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the  
25 nucleic acid of (i).

324. A vaccine comprising a vaccine vector and at least one first polypeptide selected from:

(i) a polypeptide of any one of SEQ ID Nos: 68 to 71;  
and

(ii) a polypeptide as defined in (i) which has been  
modified by conservative substitution, wherein the modified  
5 polypeptide retains immunogenicity and is at least 75%  
identical in amino acid sequence to the corresponding  
polypeptide encoded by the nucleic acid of (i).

325. A vaccine comprising a vaccine vector and at least  
one first nucleic acid selected from any one of:

10 (i) SEQ ID No: 19;

(ii) a nucleic acid sequence which encodes a  
polypeptide encoded by SEQ ID No: 19;

(iii) a nucleic acid sequence which encodes a  
polypeptide which is at least 75% identical in amino acid  
15 sequence to the polypeptide encoded by SEQ ID No: 19; and

(iv) a nucleic acid sequence which encodes a  
polypeptide whose sequence is set forth in SEQ ID No: 20;

(v) a nucleic acid sequence as defined in (i), (ii)  
or (iv), which has been modified to encode a modified  
20 polypeptide, wherein the modified polypeptide retains  
immunogenicity and is at least 75% identical in amino acid  
sequence to the corresponding polypeptide encoded by the  
nucleic acid of (i), (ii) or (iv);

wherein each first nucleic acid is capable of being  
25 expressed.

326. A vaccine comprising a vaccine vector and at least  
one first nucleic acid selected from any one of:

(i) a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 19;

(ii) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 20;

(iii) a nucleic acid sequence as defined in (i) or (ii), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding fragment of (i) or (ii);

wherein each first nucleic acid is capable of being expressed.

327. A vaccine comprising a vaccine vector and at least one first nucleic acid encoding a fusion protein, wherein the fusion protein comprises:

(a) a first polypeptide encoded by a nucleic acid selected from any one of:

(i) SEQ ID No: 19;

(ii) a nucleic acid sequence which encodes a polypeptide encoded by SEQ ID No: 19;

(iii) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by SEQ ID No: 19; and

(iv) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in SEQ ID No: 20;

(v) a nucleic acid sequence as defined in (i), (ii) or (iv), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains

immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iv); and

(b) a second polypeptide;

5 wherein each first nucleic acid is capable of being expressed.

328. A vaccine comprising a vaccine vector and at least one first nucleic acid encoding a fusion protein, wherein the fusion protein comprises:

(a) a first polypeptide encoded by a nucleic acid  
10 selected from any one of:

(i) a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 19;

(ii) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino  
15 acids from SEQ ID No: 20;

(iii) a nucleic acid sequence as defined in (i) or (ii), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the  
20 corresponding fragment of (i) or (ii); and

(b) a second polypeptide;

wherein each first nucleic acid is capable of being expressed.

329. The vaccine of claim 327 or 328 wherein the second  
25 polypeptide is a heterologous signal peptide.

330. The vaccine of claim 327 or 328 wherein the second polypeptide has adjuvant activity.

331. The vaccine of any one of claims 325 to 330 wherein wherein each first nucleic acid is operatively linked to one or more expression control sequences.

332. A vaccine according to any one of claims 325 to 331,  
5 further comprising a second nucleic acid encoding an additional polypeptide which enhances the immune response to the polypeptide expressed by the first nucleic acid.

333. The vaccine of claim 332 wherein the second nucleic acid encodes an additional *Chlamydia* polypeptide.

10 334. A pharmaceutical composition comprising a vaccine according to any one of claims 325 to 333 and a pharmaceutically acceptable carrier.

335. A fusion protein comprising a first and a second polypeptide, wherein the first polypeptide is selected from any  
15 one of:

(i) a polypeptide encoded by SEQ ID NO: 19;

(ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 20 or to the polypeptide encoded by SEQ ID NO: 19;

20 (iii) a polypeptide of SEQ ID NO: 20; and

(iv) a polypeptide as defined in (i), (ii) or (iii) which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i),  
25 (ii) or (iii).

336. A fusion protein comprising a first and a second polypeptide, wherein the first polypeptide is selected from any one of:

(i) a polypeptide encoded by a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 19;

(ii) a polypeptide which is an immunogenic fragment  
5 comprising at least 12 consecutive amino acids from SEQ ID No: 20;

(iii) a polypeptide as defined in (i) or (ii), which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding  
10 polypeptide of (i) or (ii).

337. The fusion protein of claim 335 or 336 wherein the second polypeptide is a heterologous signal peptide.

338. The fusion protein of claim 335 or 336 wherein the second polypeptide has adjuvant activity.

15 339. An antibody against the fusion protein of any one of claims 335 to 337.

340. A vaccine comprising at least one first polypeptide selected from any one of:

(i) a polypeptide encoded by SEQ ID NO: 19;

20 (ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 20 or to the polypeptide encoded by SEQ ID NO: 19;

(iii) a polypeptide of SEQ ID NO: 20; and

(iv) a polypeptide as defined in (i), (ii) or (iii)  
25 which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iii).

341. A vaccine comprising at least one first polypeptide selected from any one of:

(i) a polypeptide encoded by a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO:  
5 19;

(ii) a polypeptide which is an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No:  
20;

(iii) a polypeptide as defined in (i) or (ii), which  
10 has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) or (ii).

342. A vaccine comprising at least one fusion protein, wherein the fusion protein comprises a first and a second  
15 polypeptide, wherein the first polypeptide is selected from any one of:

(i) a polypeptide encoded by SEQ ID NO: 19;

(ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 20 or to the polypeptide  
20 encoded by SEQ ID NO: 19;

(iii) a polypeptide of SEQ ID NO: 20; and

(iv) a polypeptide as defined in (i), (ii) or (iii) which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the  
25 corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iii).

343. A vaccine comprising at least one fusion protein, wherein the fusion protein comprises a first and a second

polypeptide, wherein the first polypeptide is selected from any one of:

(i) a polypeptide encoded by a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO:

5 19;

(ii) a polypeptide which is an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 20;

(iii) a polypeptide as defined in (i) or (ii), which  
10 has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) or (ii).

344. The vaccine of claim 342 or 343 wherein the second polypeptide is a heterologous signal peptide.

15 345. The vaccine of claim 342 or 343 wherein the second polypeptide has adjuvant activity.

346. A vaccine according to any one of claims 340 to 345, further comprising an additional polypeptide which enhances the immune response to the first polypeptide.

20 347. The vaccine according to claim 346 wherein the additional polypeptide comprises a *Chlamydia* polypeptide.

348. A pharmaceutical composition comprising a vaccine according to any one of claims 340 to 347 and a pharmaceutically acceptable carrier.

25 349. A pharmaceutical composition comprising an antibody according to claim 339 and a pharmaceutically acceptable carrier.



350. A method for preventing or treating *Chlamydia* infection comprising administering to a mammal an effective amount of the vaccine of any one of claims 325 to 333 and 340 to 347.

5 351. A method for preventing or treating *Chlamydia* infection comprising administering to a mammal an effective amount of the composition of any one of claims 334, 348 and 349.

352. A method for preventing or treating *Chlamydia*  
10 infection comprising administering to a mammal an effective amount of the fusion protein of any one of claims 335 to 338.

353. A method for preventing or treating *Chlamydia* infection comprising administering to a mammal an effective amount of the antibody of claim 339.

15 354. A commercial package comprising at least one nucleic acid selected from any one of:

(i) SEQ ID No: 19;

(ii) a nucleic acid sequence which encodes a polypeptide encoded by SEQ ID No: 19;

20 (iii) a nucleic acid sequence which encodes a polypeptide which is at least 75% identical in amino acid sequence to the polypeptide encoded by SEQ ID No: 19; and

(iv) a nucleic acid sequence which encodes a polypeptide whose sequence is set forth in SEQ ID No: 20;

25 (v) a nucleic acid sequence as defined in (i), (ii) or (iv), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid

sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iv);

wherein each first nucleic acid is capable of being expressed; and

5 instructions for use in eliciting an immunoprotective response in a mammal.

355. A commercial package comprising at least one nucleic acid selected from any one of:

(i) a nucleic acid sequence comprising at least 36  
10 consecutive nucleotides from SEQ ID NO: 19;

(ii) a nucleic acid sequence which encodes an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 20;

(iii) a nucleic acid sequence as defined in (i) or  
15 (ii), which has been modified to encode a modified polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding fragment of (i) or (ii);

wherein each first nucleic acid is capable of being  
20 expressed; and

instructions for use in eliciting an immunoprotective response in a mammal.

356. A commercial package comprising at least one polypeptide selected from any one of:

25 (i) a polypeptide encoded by SEQ ID NO: 19;

(ii) a polypeptide which is at least 75% identical in amino acid sequence to SEQ ID NO: 20 or to the polypeptide encoded by SEQ ID NO: 19;

(iii) a polypeptide of SEQ ID NO: 20; and

5           (iv) a polypeptide as defined in (i), (ii) or (iii) which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i), (ii) or (iii); and

10           instructions for use in eliciting an immunoprotective response in a mammal.

357.       A commercial package comprising at least one polypeptide selected from any one of:

15           (i) a polypeptide encoded by a nucleic acid sequence comprising at least 36 consecutive nucleotides from SEQ ID NO: 19;

          (ii) a polypeptide which is an immunogenic fragment comprising at least 12 consecutive amino acids from SEQ ID No: 20;

20           (iii) a polypeptide as defined in (i) or (ii), which has been modified without loss of immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide of (i) or (ii); and

          instructions for use in eliciting an immunoprotective  
25   response in a mammal.

358.       Expression plasmid pCACPNM708 as shown in Figure 30.

359.       A vaccine comprising a vaccine vector and at least one first nucleic acid selected from:

(i) a nucleic acid encoding a polypeptide of any one of SEQ ID Nos: 72 to 74; and

(ii) a nucleic acid sequence as defined in (i) which has been modified to encode a modified conservatively substituted polypeptide, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i).

360. A vaccine comprising a vaccine vector and at least one first polypeptide selected from:

(i) a polypeptide of any one of SEQ ID Nos: 72 to 74; and

(ii) a polypeptide as defined in (i) which has been modified by conservative substitution, wherein the modified polypeptide retains immunogenicity and is at least 75% identical in amino acid sequence to the corresponding polypeptide encoded by the nucleic acid of (i).

1/111

**Figure 1. Sequence of *C. pneumoniae* ATP-binding cassette gene (SEQ ID NO: 1 and 2)**

aaatctattc ccccatogac taaatccacc acggactcgg acctcccatg tcttcaatcc																60
atatgaacgt aatattaagt agcaaattga gtactatata atg aag atg cat agg																115
Met Lys Met His Arg																
1 5																
ctt aaa cct acc tta aaa agt ctg atc cct aat ctt ctt ttc tta ttg																163
Leu Lys Pro Thr Leu Lys Ser Leu Ile Pro Asn Leu Leu Phe Leu Leu																
10 15 20																
ctc act ctt tca agc tgc tca aag caa aaa caa gaa ccc tta gga aaa																211
Leu Thr Leu Ser Ser Cys Ser Lys Gln Lys Gln Glu Pro Leu Gly Lys																
25 30 35																
cat ctc gtt att gcg atg agc cat gat ctc gcc gac cta gat cct cgc																259
His Leu Val Ile Ala Met Ser His Asp Leu Ala Asp Leu Asp Pro Arg																
40 45 50																
aat gcc tat tta agc aga gat gct tcc cta gca aaa gcc ctc tat gaa																307
Asn Ala Tyr Leu Ser Arg Asp Ala Ser Leu Ala Lys Ala Leu Tyr Glu																
55 60 65																
gga ctg aca aga gaa act gat caa gga atc gca ctg gct ctt gca gaa																355
Gly Leu Thr Arg Glu Thr Asp Gln Gly Ile Ala Leu Ala Leu Ala Glu																
70 75 80 85																
agt tat acc ctg tca aaa gat cat aag gtc tat acc ttt aaa ctc aga																403
Ser Tyr Thr Leu Ser Lys Asp His Lys Val Tyr Thr Phe Lys Leu Arg																
90 95 100																
cct tct gtg tgg agc gat ggc act cca ctc act gct tat gac ttt gaa																451
Pro Ser Val Trp Ser Asp Gly Thr Pro Leu Thr Ala Tyr Asp Phe Glu																
105 110 115																
aaa tct ata aaa caa ctg tac ttc gaa gaa ttt tca cct tcc ata cat																499
Lys Ser Ile Lys Gln Leu Tyr Phe Glu Glu Phe Ser Pro Ser Ile His																
120 125 130																
act tta ctc ggc gtg att aaa aat tct tcg gca atc cac aat gct caa																547
Thr Leu Leu Gly Val Ile Lys Asn Ser Ser Ala Ile His Asn Ala Gln																
135 140 145																
aaa tct ctg gaa act ctt ggg ata cag gca aaa gat gat ctt act ttg																595
Lys Ser Leu Glu Thr Leu Gly Ile Gln Ala Lys Asp Asp Leu Thr Leu																
150 155 160 165																
gtg att acc cta gag caa cct ttc cca tac ttt ctc aca ctt atc gct																643
Val Ile Thr Leu Glu Gln Pro Phe Pro Tyr Phe Leu Thr Leu Ile Ala																
170 175 180																

2/111

Figure 1 (Cont.)

cgc ccc gta ttc tcc cct gtt cat cac acc ctt agg gaa tcc tat aag	691
Arg Pro Val Phe Ser Pro Val His His Thr Leu Arg Glu Ser Tyr Lys	
185 190 195	
aaa gga aca ccc cca tcc aca tac atc tcc aat ggg ccc ttt gtc tta	739
Lys Gly Thr Pro Pro Ser Thr Tyr Ile Ser Asn Gly Pro Phe Val Leu	
200 205 210	
aaa aaa cat gaa cac caa aac tac tta att tta gaa aaa aat cct cac	787
Lys Lys His Glu His Gln Asn Tyr Leu Ile Leu Glu Lys Asn Pro His	
215 220 225	
tac tat gat cat gaa tca gta aag tta gac cga gtc acc tta aaa att	835
Tyr Tyr Asp His Glu Ser Val Lys Leu Asp Arg Val Thr Leu Lys Ile	
230 235 240 245	
atc cca gac gcc tcc aca gcc acg aaa ctt ttc aaa agt aaa tct ata	883
Ile Pro Asp Ala Ser Thr Ala Thr Lys Leu Phe Lys Ser Lys Ser Ile	
250 255 260	
gat tgg att ggc tca cct tgg agc gct ccg ata tct aac gaa gac caa	931
Asp Trp Ile Gly Ser Pro Trp Ser Ala Pro Ile Ser Asn Glu Asp Gln	
265 270 275	
aaa gtt ctc tcc caa gaa aag att ctt acc tat tct gtt tca agc acc	979
Lys Val Leu Ser Gln Glu Lys Ile Leu Thr Tyr Ser Val Ser Ser Thr	
280 285 290	
acc ctt ctt atc tat aac ctg caa aaa cct cta ata caa aat aaa gcc	1027
Thr Leu Leu Ile Tyr Asn Leu Gln Lys Pro Leu Ile Gln Asn Lys Ala	
295 300 305	
ctc agg aaa gcc att gct cat gct att gat aga aaa tct atc tta aga	1075
Leu Arg Lys Ala Ile Ala His Ala Ile Asp Arg Lys Ser Ile Leu Arg	
310 315 320 325	
ctc gtg cct tca gga caa gaa gct gta act cta gtt ccc cca aat ctt	1123
Leu Val Pro Ser Gly Gln Glu Ala Val Thr Leu Val Pro Pro Asn Leu	
330 335 340	
tca caa ctc aat ctt caa aaa gag atc tca aca gaa gaa cga caa aca	1171
Ser Gln Leu Asn Leu Gln Lys Glu Ile Ser Thr Glu Glu Arg Gln Thr	
345 350 355	
aaa gcc aga gca tat ttt caa gaa gct aaa gaa aca ctt tct gaa aaa	1219
Lys Ala Arg Ala Tyr Phe Gln Glu Ala Lys Glu Thr Leu Ser Glu Lys	
360 365 370	
gaa ctc gca gaa ctc agc atc ctc tat cct ata gat tcc tcg aat tcc	1267
Glu Leu Ala Glu Leu Ser Ile Leu Tyr Pro Ile Asp Ser Ser Asn Ser	
375 380 385	

3/111

Figure 1 (Cont.)

tcc atc ata gct caa gaa atc caa aga caa ctt aaa gat acc tta gga	1315
Ser Ile Ile Ala Gln Glu Ile Gln Arg Gln Leu Lys Asp Thr Leu Gly	
390 395 400 405	
ttg aaa atc aaa atc caa ggc atg gag tac cac tgc ttt tta aag aaa	1363
Leu Lys Ile Lys Ile Gln Gly Met Glu Tyr His Cys Phe Leu Lys Lys	
410 415 420	
cgt cgt caa gga gat ttc ttc ata gcg aca gga gga tgg att gcg gaa	1411
Arg Arg Gln Gly Asp Phe Phe Ile Ala Thr Gly Gly Trp Ile Ala Glu	
425 430 435	
tac gta agc ccc gta gcc ttc cta tct att cta ggc aac ccc aga gac	1459
Tyr Val Ser Pro Val Ala Phe Leu Ser Ile Leu Gly Asn Pro Arg Asp	
440 445 450	
ctc aca caa tgg aga aac agt gat tac gaa aag act tta gag aaa ctc	1507
Leu Thr Gln Trp Arg Asn Ser Asp Tyr Glu Lys Thr Leu Glu Lys Leu	
455 460 465	
tat ctc cct cat gcc tac aaa gag aat tta aaa cgc gca gaa atg ata	1555
Tyr Leu Pro His Ala Tyr Lys Glu Asn Leu Lys Arg Ala Glu Met Ile	
470 475 480 485	
ata gaa gaa gaa acc ccg att atc ccc ctg tat cac ggc aaa tat att	1603
Ile Glu Glu Glu Thr Pro Ile Ile Pro Leu Tyr His Gly Lys Tyr Ile	
490 495 500	
tac gct ata cat cct aaa atc cag aat aca ttc gga tct ctt cta ggc	1651
Tyr Ala Ile His Pro Lys Ile Gln Asn Thr Phe Gly Ser Leu Leu Gly	
505 510 515	
cac aca gat ctc aaa aat atc gat atc tta agt tagatccgaa atggaaaaat	1704
His Thr Asp Leu Lys Asn Ile Asp Ile Leu Ser	
520 525	
taaaaatttt atagacaatc ttgaaaagag aattaaat ttttaattta aattatagtt	1764
gcaattgaaa acgcccctaa gaa	1787

4/111

**Figure 2. Sequence of *C. pneumoniae* secretory locus ORF gene (SEQ ID NO: 3 and 4).**

```

ttccagagaa atcctgatcc tgaaaaactt cctgaaacaa ttgctttaac tataaacacgg 60
gaacctaaag catatcctcc aaggacgtta acataccaat ttg cgg ttg gga aat 115
                                         Leu Arg Leu Gly Asn
                                         1           5

aag cct atg caa cct ttt atc ttt act tta ctg tgc ttg aca tct ttg 163
Lys Pro Met Gln Pro Phe Ile Phe Thr Leu Leu Cys Leu Thr Ser Leu
                        10                15                20

gtt tct tta gtc gcc ttt gat gct gcg aat gct cgt aaa cgt tgt gcc 211
Val Ser Leu Val Ala Phe Asp Ala Ala Asn Ala Arg Lys Arg Cys Ala
                        25                30                35

tgt gct caa act ata gaa cgt gga gag aac ttc ttt tcc ata aaa cgc 259
Cys Ala Gln Thr Ile Glu Arg Gly Glu Asn Phe Phe Ser Ile Lys Arg
                        40                45                50

tct gct tgt gct gaa atc gaa tat caa gaa aaa tct cgc cac gcc tca 307
Ser Ala Cys Ala Glu Ile Glu Tyr Gln Glu Lys Ser Arg His Ala Ser
                        55                60                65

gca att gaa aga atc tca aaa gat aaa ggc aaa gtc act cca aag cag 355
Ala Ile Glu Arg Ile Ser Lys Asp Lys Gly Lys Val Thr Pro Lys Gln
                        70                75                80                85

att gcg aaa gta gct act aag aaa aag caa aga tac cgt tta ttg cag 403
Ile Ala Lys Val Ala Thr Lys Lys Lys Gln Arg Tyr Arg Leu Leu Gln
                        90                95                100

gtt cct ttt tca agg cct ccg aat aac tca agg tat aac ctc tat gct 451
Val Pro Phe Ser Arg Pro Pro Asn Asn Ser Arg Tyr Asn Leu Tyr Ala
                        105                110                115

ttg ctt agt gaa cct ccc gaa tgc tat agc gat aca gca tca tgg tat 499
Leu Leu Ser Glu Pro Pro Glu Cys Tyr Ser Asp Thr Ala Ser Trp Tyr
                        120                125                130

gct att ttt att cgg tta ctt cga cgt gct tat gta gac acg gga aat 547
Ala Ile Phe Ile Arg Leu Leu Arg Arg Ala Tyr Val Asp Thr Gly Asn
                        135                140                145

gta cct cct gga tct gag tat gcc atc gct aat gct ttg ata agt aac 595
Val Pro Pro Gly Ser Glu Tyr Ala Ile Ala Asn Ala Leu Ile Ser Asn
                        150                155                160                165

aaa caa gag att tta gag agg gga gcg cag ctt gga ccc gat gtt att 643
Lys Gln Glu Ile Leu Glu Arg Gly Ala Gln Leu Gly Pro Asp Val Ile
                        170                175                180

```



5/111

Figure 2 (Cont.)

gaa act cta aca ttg cct gag gaa caa gcc gag att ttt tat aaa atg	691
Glu Thr Leu Thr Leu Pro Glu Glu Gln Ala Glu Ile Phe Tyr Lys Met	
185 190 195	
ctc aaa ggg tcg tca aac tct cag tcg cta ctg aat ttt ctg cat tat	739
Leu Lys Gly Ser Ser Asn Ser Gln Ser Leu Leu Asn Phe Leu His Tyr	
200 205 210	
gaa gag aaa agc tta ggc cac tgt aag cta aat ctg atc ttc atg gat	787
Glu Glu Lys Ser Leu Gly His Cys Lys Leu Asn Leu Ile Phe Met Asp	
215 220 225	
ccc cta ctg tta gaa gct gtt cta gat cat ccc gat gct tat agg gaa	835
Pro Leu Leu Leu Glu Ala Val Leu Asp His Pro Asp Ala Tyr Arg Glu	
230 235 240 245	
acg tcg ctc ctg cgc gat ggc att tgg gaa gcg gtg aag cgt caa gaa	883
Thr Ser Leu Leu Arg Asp Gly Ile Trp Glu Ala Val Lys Arg Gln Glu	
250 255 260	
cat gcc atc caa gaa cat ggc cag gca gct gct ttg gag ctt ttt aaa	931
His Ala Ile Gln Glu His Gly Gln Ala Ala Ala Leu Glu Leu Phe Lys	
265 270 275	
aca cgc acc gac ttc cgc ctg gag ctg cga gat aag atg cag tta ctt	979
Thr Arg Thr Asp Phe Arg Leu Glu Leu Arg Asp Lys Met Gln Leu Leu	
280 285 290	
cta agt cga tac gat ttg ctc ccc tta tta aat aaa aaa atg ttc gac	1027
Leu Ser Arg Tyr Asp Leu Leu Pro Leu Leu Asn Lys Lys Met Phe Asp	
295 300 305	
tac acc tta gga agt gcc gga gat tac tta ttt ttg gta gac cca gat	1075
Tyr Thr Leu Gly Ser Ala Gly Asp Tyr Leu Phe Leu Val Asp Pro Asp	
310 315 320 325	
act aag gca att tct cga tgt cgc tgc cct tca aag agt att aaa tta	1123
Thr Lys Ala Ile Ser Arg Cys Arg Cys Pro Ser Lys Ser Ile Lys Leu	
330 335 340	
taattttaatt ttaatatatta ttttaaataag ttttttttga taattgtctt aataagtaact	1183
ataaaaaata tttctatagg taggaccatg gcagacgaga ccc	1226

6/111

**Figure 3. Sequence of *C. pneumoniae* Endopeptidase gene (SEQ ID NO: 5 and 6).**

```

gttacttttt ttttcataaa aaccccatgt aacttttact tgctcatatt gagaagtccc 60
ccatactata aaaggcaacg ttttcttttc ttgggttttt atg ctc acc cta ggc 115
                                     Met Leu Thr Leu Gly
                                     1 5

ttg gaa agt tct tgc gat gag act gcc tgc gct ata gtt aat gag gat 163
Leu Glu Ser Ser Cys Asp Glu Thr Ala Cys Ala Ile Val Asn Glu Asp
                        10 15 20

aag cag ata tta gca aat att att gcc tct caa gat atc cat gca tcc 211
Lys Gln Ile Leu Ala Asn Ile Ile Ala Ser Gln Asp Ile His Ala Ser
                        25 30 35

tat ggc gga gtc gtt cct gaa ctt gct tca aga gca cat ctc cat atc 259
Tyr Gly Gly Val Val Pro Glu Leu Ala Ser Arg Ala His Leu His Ile
                        40 45 50

ttc cca caa gtg ata aat aaa gct cta caa cag gcc aac tta ttg atc 307
Phe Pro Gln Val Ile Asn Lys Ala Leu Gln Gln Ala Asn Leu Leu Ile
                        55 60 65

gaa gat atg gat ctg att gca gta acg caa act cca ggg ttg ata ggt 355
Glu Asp Met Asp Leu Ile Ala Val Thr Gln Thr Pro Gly Leu Ile Gly
                        70 75 80 85

tct cta tca gta gga gtg cat ttt ggt aaa ggc att gcc ata gga gca 403
Ser Leu Ser Val Gly Val His Phe Gly Lys Gly Ile Ala Ile Gly Ala
                        90 95 100

aaa aaa tcc ttg att gga gtc aat cac gtc gaa gct cat ctc tat gct 451
Lys Lys Ser Leu Ile Gly Val Asn His Val Glu Ala His Leu Tyr Ala
                        105 110 115

gcc tat atg gca gcg caa aac gtg caa ttc cct gct tta ggt ctt gtg 499
Ala Tyr Met Ala Ala Gln Asn Val Gln Phe Pro Ala Leu Gly Leu Val
                        120 125 130

gtc tct gga gct cat acc gca gcg ttt ttt ata gaa aat cct aca tcc 547
Val Ser Gly Ala His Thr Ala Ala Phe Phe Ile Glu Asn Pro Thr Ser
                        135 140 145

tat aaa ctc ata gga aaa act cga gat gat gct ata gga gaa act ttt 595
Tyr Lys Leu Ile Gly Lys Thr Arg Asp Asp Ala Ile Gly Glu Thr Phe
                        150 155 160 165

gat aaa gta gga cgc ttt cta gga tta cca tac cct gca ggc cca tta 643
Asp Lys Val Gly Arg Phe Leu Gly Leu Pro Tyr Pro Ala Gly Pro Leu
                        170 175 180

```

7/111

Figure 3 (Cont.)

att gaa aaa ctc gct tta gaa ggc tct gag gac agt tat cct ttt agt	691
Ile Glu Lys Leu Ala Leu Glu Gly Ser Glu Asp Ser Tyr Pro Phe Ser	
185 190 195	
cca gct aaa gtc cca aac tat gac ttt tca ttc agc ggt ctt aaa aca	739
Pro Ala Lys Val Pro Asn Tyr Asp Phe Ser Phe Ser Gly Leu Lys Thr	
200 205 210	
gct gtt ctc tac gca atc aaa gga aat aat agt agc ccc cgc tct cct	787
Ala Val Leu Tyr Ala Ile Lys Gly Asn Asn Ser Ser Pro Arg Ser Pro	
215 220 225	
gct cca gag ata tct tta gaa aaa caa aga gat atc gct gct tca ttt	835
Ala Pro Glu Ile Ser Leu Glu Lys Gln Arg Asp Ile Ala Ala Ser Phe	
230 235 240 245	
caa aaa gcg gcc tgc act act att gca caa aaa ctt ccc act att ata	883
Gln Lys Ala Ala Cys Thr Thr Ile Ala Gln Lys Leu Pro Thr Ile Ile	
250 255 260	
aaa gaa ttt tcg tgc cga tct ata ctt att gga ggt ggc gta gcc att	931
Lys Glu Phe Ser Cys Arg Ser Ile Leu Ile Gly Gly Gly Val Ala Ile	
265 270 275	
aat gaa tac ttt aga tcc gca ata caa act gcg tgt aat cta cct gta	979
Asn Glu Tyr Phe Arg Ser Ala Ile Gln Thr Ala Cys Asn Leu Pro Val	
280 285 290	
tac ttc ccc cct gct aaa cta tgc tca gat aat gct gct atg att gca	1027
Tyr Phe Pro Pro Ala Lys Leu Cys Ser Asp Asn Ala Ala Met Ile Ala	
295 300 305	
ggt cta ggg gga gaa aat ttt caa aaa aac tct agt att ccg gaa att	1075
Gly Leu Gly Gly Glu Asn Phe Gln Lys Asn Ser Ser Ile Pro Glu Ile	
310 315 320 325	
cgt ata tgc gca aga tat cag tgg gaa tct gta tca cca ttc tcc tta	1123
Arg Ile Cys Ala Arg Tyr Gln Trp Glu Ser Val Ser Pro Phe Ser Leu	
330 335 340	
gcc tct ccg tagtcctcca aggctgcaag gagtccagtc actcctctac	1172
Ala Ser Pro	
atctcgggga gaactcgcta ttaatatag agatgaaccc cggtcttttag atccaagaca	1232
agt	1235

8/111

**Figure 4: Sequence of *C. pneumoniae* Protease gene (SEQ ID NO: 7 and 8).**

gattttgtgt attttttcag ataatgtttt taaaaaaatg ttttaaaacc ctaaaatcct																60
acctcccttggt aaccattctc ggtagaaaag agagggtat																115
Met Lys Lys Gly Lys 1 5																
tta gga gcc ata gtt ttt ggc ctt cta ttt aca agt agt gtt gct ggt	163															
Leu Gly Ala Ile Val Phe Gly Leu Leu Phe Thr Ser Ser Val Ala Gly	10 15 20															
ttt tct aag gat ttg act aaa gac aac gct tat caa gat tta aat gtc																211
Phe Ser Lys Asp Leu Thr Lys Asp Asn Ala Tyr Gln Asp Leu Asn Val 25 30 35																
ata gag cat tta ata tcg tta aaa tat gct cct tta cca tgg aag gaa																259
Ile Glu His Leu Ile Ser Leu Lys Tyr Ala Pro Leu Pro Trp Lys Glu 40 45 50																
cta tta ttt ggt tgg gat tta tct cag caa aca cag caa gct cgc ttg																307
Leu Leu Phe Gly Trp Asp Leu Ser Gln Gln Thr Gln Gln Ala Arg Leu 55 60 65																
caa ctg gtc tta gaa gaa aaa cca aca acc aac tac tgc cag aag gta																355
Gln Leu Val Leu Glu Glu Lys Pro Thr Thr Asn Tyr Cys Gln Lys Val 70 75 80 85																
ctc tct aac tac gtg aga tca tta aac gat tat cat gca ggg att acg																403
Leu Ser Asn Tyr Val Arg Ser Leu Asn Asp Tyr His Ala Gly Ile Thr 90 95 100																
ttt tat cgt act gaa agt gcg tat atc cct tac gta ttg aag tta agt																451
Phe Tyr Arg Thr Glu Ser Ala Tyr Ile Pro Tyr Val Leu Lys Leu Ser 105 110 115																
gaa gat ggt cat gtc ttt gta gtc gac gta cag act agc caa ggg gat																499
Glu Asp Gly His Val Phe Val Val Asp Val Gln Thr Ser Gln Gly Asp 120 125 130																
att tac tta ggg gat gaa atc ctt gaa gta gat gga atg ggg att cgt																547
Ile Tyr Leu Gly Asp Glu Ile Leu Glu Val Asp Gly Met Gly Ile Arg 135 140 145																
gag gct atc gaa agc ctt cgc ttt gga cga ggg agt gcc aca gac tat																595
Glu Ala Ile Glu Ser Leu Arg Phe Gly Arg Gly Ser Ala Thr Asp Tyr 150 155 160 165																
tct gct gca gtt cgt tcc ttg aca tcg cgt tcc gcc gct ttt gga gat																643
Ser Ala Ala Val Arg Ser Leu Thr Ser Arg Ser Ala Ala Phe Gly Asp 170 175 180																

9/111

Figure 4 (Cont.)

gcg gtt cct tca gga att gcc atg ttg aaa ctt cgc cga ccc agt ggt	691
Ala Val Pro Ser Gly Ile Ala Met Leu Lys Leu Arg Arg Pro Ser Gly	
185 190 195	
ttg atc cgt tcg aca ccg gtc cgt tgg cgt tat act cca gag cat atc	739
Leu Ile Arg Ser Thr Pro Val Arg Trp Arg Tyr Thr Pro Glu His Ile	
200 205 210	
gga gat ttt tct tta gtt gct cct ttg att cct gaa cat aaa cct caa	787
Gly Asp Phe Ser Leu Val Ala Pro Leu Ile Pro Glu His Lys Pro Gln	
215 220 225	
tta cct aca caa agt tgt gtg cta ttc cgt tcc ggg gta aat tca cag	835
Leu Pro Thr Gln Ser Cys Val Leu Phe Arg Ser Gly Val Asn Ser Gln	
230 235 240 245	
tct tct agt agc tct tta ttc agt tcc tac atg gtg cct tat ttc tgg	883
Ser Ser Ser Ser Leu Phe Ser Ser Tyr Met Val Pro Tyr Phe Trp	
250 255 260	
gaa gaa ttg cgg gtt caa aat aag cag cgt ttt gac agt aat cac cat	931
Glu Glu Leu Arg Val Gln Asn Lys Gln Arg Phe Asp Ser Asn His His	
265 270 275	
ata ggg agc cgt aat gga ttt tta cct acg ttt ggt cct att ctt tgg	979
Ile Gly Ser Arg Asn Gly Phe Leu Pro Thr Phe Gly Pro Ile Leu Trp	
280 285 290	
gaa caa gac aag ggg ccc tat cgt tcc tat atc ttt aaa gca aaa gat	1027
Glu Gln Asp Lys Gly Pro Tyr Arg Ser Tyr Ile Phe Lys Ala Lys Asp	
295 300 305	
tct cag ggc aat ccc cat cgc ata gga ttt tta aga att tct tct tat	1075
Ser Gln Gly Asn Pro His Arg Ile Gly Phe Leu Arg Ile Ser Ser Tyr	
310 315 320 325	
gtt tgg act gat tta gaa gga ctt gaa gag gat cat aag gat agt cct	1123
Val Trp Thr Asp Leu Glu Gly Leu Glu Glu Asp His Lys Asp Ser Pro	
330 335 340	
tgg gag ctc ttt gga gag atc atc gat cat ttg gaa aaa gag act gat	1171
Trp Glu Leu Phe Gly Glu Ile Ile Asp His Leu Glu Lys Glu Thr Asp	
345 350 355	
gct ttg att att gat cag acc cat aat cct gga ggc agt gtt ttc tat	1219
Ala Leu Ile Ile Asp Gln Thr His Asn Pro Gly Gly Ser Val Phe Tyr	
360 365 370	
ctc tat tcg tta cta tct atg tta aca gat cat cct tta gat act cct	1267
Leu Tyr Ser Leu Leu Ser Met Leu Thr Asp His Pro Leu Asp Thr Pro	
375 380 385	

10/111

Figure 4 (Cont.)

aaa cat aga atg att ttc act cag gat gaa gtc ago tcg gct ttg cac	1315
Lys His Arg Met Ile Phe Thr Gln Asp Glu Val Ser Ser Ala Leu His	
390 395 400 405	
tggtg caa gat cta cta gaa gat gtc ttc aca gat gag cag gca gtt gcc	1363
Trp Gln Asp Leu Leu Glu Asp Val Phe Thr Asp Glu Gln Ala Val Ala	
410 415 420	
gtg cta ggg gaa act atg gaa gga tat tgc atg gat atg cat gct gta	1411
Val Leu Gly Glu Thr Met Glu Gly Tyr Cys Met Asp Met His Ala Val	
425 430 435	
gcc tct ctt caa aac ttc tct cag agt gtc ctt tct tcc tgg gtt tca	1459
Ala Ser Leu Gln Asn Phe Ser Gln Ser Val Leu Ser Ser Trp Val Ser	
440 445 450	
ggt gat att aac ctt tca aaa cct atg cct ttg cta gga ttt gca cag	1507
Gly Asp Ile Asn Leu Ser Lys Pro Met Pro Leu Leu Gly Phe Ala Gln	
455 460 465	
gtt cga cct cat cct aaa cat caa tat act aaa cct ttg ttt atg ttg	1555
Val Arg Pro His Pro Lys His Gln Tyr Thr Lys Pro Leu Phe Met Leu	
470 475 480 485	
ata gac gag gat gac ttc tct tgt gga gat tta gcg cct gca att ttg	1603
Ile Asp Glu Asp Asp Phe Ser Cys Gly Asp Leu Ala Pro Ala Ile Leu	
490 495 500	
aag gat aat ggc cgc gct act ctc att gga aag cca aca gca gga gct	1651
Lys Asp Asn Gly Arg Ala Thr Leu Ile Gly Lys Pro Thr Ala Gly Ala	
505 510 515	
gga ggt ttt gta ttc caa gtc act ttc cct aac cgt tct gga att aaa	1699
Gly Gly Phe Val Phe Gln Val Thr Phe Pro Asn Arg Ser Gly Ile Lys	
520 525 530	
ggt ctt tct tta aca gga tct tta gct gtt agg aaa gat ggt gag ttt	1747
Gly Leu Ser Leu Thr Gly Ser Leu Ala Val Arg Lys Asp Gly Glu Phe	
535 540 545	
att gaa aac tta gga gtg gct cct cat att gat tta gga ttt acc tcc	1795
Ile Glu Asn Leu Gly Val Ala Pro His Ile Asp Leu Gly Phe Thr Ser	
550 555 560 565	
agg gat ttg caa act tcc agg ttt act gat tac gtt gag gca gtg aaa	1843
Arg Asp Leu Gln Thr Ser Arg Phe Thr Asp Tyr Val Glu Ala Val Lys	
570 575 580	
act ata gtt tta act tct ttg tct gag aac gct aag aag agt gaa gag	1891
Thr Ile Val Leu Thr Ser Leu Ser Glu Asn Ala Lys Lys Ser Glu Glu	
585 590 595	

11/111

Figure 4 (Cont.)

```
cag act tct ccg caa gag acg cct gaa gtt att cga gtc tct tat ccc 1939
Gln Thr Ser Pro Gln Glu Thr Pro Glu Val Ile Arg Val Ser Tyr Pro
      600                      605                      610

aca acg act tct gct tcg taaacgggac gtaatagaat aatttttatt 1987
Thr Thr Thr Ser Ala Ser
      615

attgctttaa tatgcgcgct tccaatataa gcattgtgaa gcgcgtttca tatgtctttt 2047

atcttttaggt aat 2060
```

12/111

**Figure 5. Sequence of *C. pneumoniae* Metalloprotease gene (SEQ ID NO: 9 and 10).**

```

gacgtaatag aataattttt attattgctt taatatgcgc gcttccaata taagcattgt 60
gaagcgcggtt tcatatgtct tttatcttta ggtaattatt atg aga aaa ctt att 115
                                     Met Arg Lys Leu Ile
                                     1 5
tta tgc aat cct aga gga ttt tgc tct gga gtt gtg cgc gct att caa 163
Leu Cys Asn Pro Arg Gly Phe Cys Ser Gly Val Val Arg Ala Ile Gln
                                     10 15 20
ggt gta gag gtt gct tta gaa aag tgg gga gct cct atc tat gta aaa 211
Val Val Glu Val Ala Leu Glu Lys Trp Gly Ala Pro Ile Tyr Val Lys
                                     25 30 35
cat gag att gtt cac aat cgc cat gtt gtt aat gct tta cga gcc aag 259
His Glu Ile Val His Asn Arg His Val Val Asn Ala Leu Arg Ala Lys
                                     40 45 50
gga gcg atc ttt gtt gaa gaa ctt gtt gat gtt cct gaa ggt gag aga 307
Gly Ala Ile Phe Val Glu Glu Leu Val Asp Val Pro Glu Gly Glu Arg
                                     55 60 65
gtc att tat tca gct cat gga att cct cct tca gtt aga gct gaa gca 355
Val Ile Tyr Ser Ala His Gly Ile Pro Pro Ser Val Arg Ala Glu Ala
                                     70 75 80 85
aaa gcc cgt aag ctt att gat att gat gct acc tgt ggt ttg gtt act 403
Lys Ala Arg Lys Leu Ile Asp Ile Asp Ala Thr Cys Gly Leu Val Thr
                                     90 95 100
aag gtg cat tct gct gcg aag tta tac gca agt aaa gga tac aaa atc 451
Lys Val His Ser Ala Ala Lys Leu Tyr Ala Ser Lys Gly Tyr Lys Ile
                                     105 110 115
ata ctg atc ggc cat aag aag cac gtt gag gtg att ggt att gtt gga 499
Ile Leu Ile Gly His Lys Lys His Val Glu Val Ile Gly Ile Val Gly
                                     120 125 130
gaa gtt cct gaa cac att act gtt gtc gag aag gtt gct gac gtc gag 547
Glu Val Pro Glu His Ile Thr Val Val Glu Lys Val Ala Asp Val Glu
                                     135 140 145
gcc tta cct ttt agt tct gat aca cct tta ttt tat att act caa acg 595
Ala Leu Pro Phe Ser Ser Asp Thr Pro Leu Phe Tyr Ile Thr Gln Thr
                                     150 155 160 165
acg ttg agt ttg gat gat gtt cag gag atc tca tcg gct ttg cta aag 643
Thr Leu Ser Leu Asp Asp Val Gln Glu Ile Ser Ser Ala Leu Leu Lys
                                     170 175 180

```



13/111

Figure 5 (Cont.)

cga tat ccc tct atc att act ctg cct agt tct tcg att tgt tat gca	691
Arg Tyr Pro Ser Ile Ile Thr Leu Pro Ser Ser Ser Ile Cys Tyr Ala	
185 190 195	
acc acg aac cgt caa aaa gca ttg cgt tct gtt tta tct cgc gtg aat	739
Thr Thr Asn Arg Gln Lys Ala Leu Arg Ser Val Leu Ser Arg Val Asn	
200 205 210	
tac gtc tat gtg gtt gga gat gtc aac agc tcg aat tcc aat cgt ctt	787
Tyr Val Tyr Val Val Gly Asp Val Asn Ser Ser Asn Ser Asn Arg Leu	
215 220 225	
cgc gaa gtg gct ttg aga agg gga gtt ccc gct gat ttg atc aac aat	835
Arg Glu Val Ala Leu Arg Arg Gly Val Pro Ala Asp Leu Ile Asn Asn	
230 235 240 245	
ccc gag gat att gat acg aac atc gta aat cat tct gga gat ata gca	883
Pro Glu Asp Ile Asp Thr Asn Ile Val Asn His Ser Gly Asp Ile Ala	
250 255 260	
atg act gca gga gcc tca act ccc gaa gac gta gtt caa gct tgc att	931
Met Thr Ala Gly Ala Ser Thr Pro Glu Asp Val Val Gln Ala Cys Ile	
265 270 275	
cga aag cta tca tca ctt atc cct ggt tta caa gtg gaa aat gat ata	979
Arg Lys Leu Ser Ser Leu Ile Pro Gly Leu Gln Val Glu Asn Asp Ile	
280 285 290	
ttt gct gta gag gat gtc gta ttt caa tta cca aaa gaa ctc cgt tgt	1027
Phe Ala Val Glu Asp Val Val Phe Gln Leu Pro Lys Glu Leu Arg Cys	
295 300 305	
tct taggtcttta ggcttacttg ccaagttttt ctcgagattg ctttatagag	1080
Ser	
310	
tcttcttctc gttcagagag ggtattttacc tttttagttc tctgtatttg aaa	1133

14/111

**Figure 6. Sequence of *C. pneumoniae* CLP protease ATPase gene (SEQ ID NOS 11 and 12).**

catggggagcc gaggaagcca tctcctacgg acttattgat aaggtggtaa cttctgcgaa															60
agaaactaat aaggatacaa gtagcactta gagagaacat atg aat aaa aaa aat															115
Met Asn Lys Lys Asn															5
1															
cta act att tgt tca ttt tgc ggt cgg tct gaa aaa gat gta gag aaa															163
Leu Thr Ile Cys Ser Phe Cys Gly Arg Ser Glu Lys Asp Val Glu Lys															20
10															
ctg att got ggg cct tcg gta tac att tgt gac tac tgc atc aaa tta															211
Leu Ile Ala Gly Pro Ser Val Tyr Ile Cys Asp Tyr Cys Ile Lys Leu															35
25															
30															
35															
tgc tct gga att tta gat aag aaa ccc tcc tct aca ata tcc tca gct															259
Cys Ser Gly Ile Leu Asp Lys Lys Pro Ser Ser Thr Ile Ser Ser Ala															50
40															
45															
50															
cca gtt tct gaa aca cct tca cag cct tct gat ctg agg gtg ctt acc															307
Pro Val Ser Glu Thr Pro Ser Gln Pro Ser Asp Leu Arg Val Leu Thr															65
55															
60															
65															
cct aag gaa atc aaa aag cat att gat gaa tat gtc att ggt cag gaa															355
Pro Lys Glu Ile Lys Lys His Ile Asp Glu Tyr Val Ile Gly Gln Glu															85
70															
75															
80															
85															
aga gct aaa aag aca atc gct gtt gct gtt tat aat cac tat aaa cgt															403
Arg Ala Lys Lys Thr Ile Ala Val Ala Val Tyr Asn His Tyr Lys Arg															100
90															
95															
100															
ata cgt gct cta cta cat aac aaa cag gta agc tac ggg aaa tct aac															451
Ile Arg Ala Leu Leu His Asn Lys Gln Val Ser Tyr Gly Lys Ser Asn															115
105															
110															
115															
gtg ctt ctg cta ggc cct aca gga tct gga aaa aca tta att gca aaa															499
Val Leu Leu Leu Gly Pro Thr Gly Ser Gly Lys Thr Leu Ile Ala Lys															130
120															
125															
130															
135															
140															
145															
150															
155															
160															
165															
acc cta acg gaa gca ggt tat gtc ggt gaa gat gta gag aac att gtc															595
Thr Leu Thr Glu Ala Gly Tyr Val Gly Glu Asp Val Glu Asn Ile Val															165

15/111

Figure 6 (Cont.)

tta cgt tta tta caa gct gct gat tac gat gtc gcc cgt gca gaa cga	643
Leu Arg Leu Leu Gln Ala Ala Asp Tyr Asp Val Ala Arg Ala Glu Arg	
170 175 180	
ggc att atc tat atc gat gaa atc gat aaa att gga agg aca aca gca	691
Gly Ile Ile Tyr Ile Asp Glu Ile Asp Lys Ile Gly Arg Thr Thr Ala	
185 190 195	
aac gtc tcc att act aga gat gtt tct ggc gaa ggg gtt caa caa gca	739
Asn Val Ser Ile Thr Arg Asp Val Ser Gly Glu Gly Val Gln Gln Ala	
200 205 210	
ttg tta aaa atc gtt gaa gga acc aca gca aac gtt cct cct aaa gga	787
Leu Leu Lys Ile Val Glu Gly Thr Thr Ala Asn Val Pro Pro Lys Gly	
215 220 225	
gga cgt aag cat cct aac caa gag tat atc cga gtc aat acg gaa aat	835
Gly Arg Lys His Pro Asn Gln Glu Tyr Ile Arg Val Asn Thr Glu Asn	
230 235 240 245	
atc tta ttt atc gta ggc gga gcc ttc gtc aac cta gat aag att atc	883
Ile Leu Phe Ile Val Gly Gly Ala Phe Val Asn Leu Asp Lys Ile Ile	
250 255 260	
gca aag cga ttg ggg aaa act acc ata ggg ttt tct gat gat caa gca	931
Ala Lys Arg Leu Gly Lys Thr Thr Ile Gly Phe Ser Asp Asp Gln Ala	
265 270 275	
gac ctc tct caa aaa acc aga gac cat cta ctt gct aaa gtt gaa acc	979
Asp Leu Ser Gln Lys Thr Arg Asp His Leu Leu Ala Lys Val Glu Thr	
280 285 290	
gaa gac ctg att gcc ttc gga atg atc cct gaa ttt gtc gga aga ttc	1027
Glu Asp Leu Ile Ala Phe Gly Met Ile Pro Glu Phe Val Gly Arg Phe	
295 300 305	
aac tgc att gta aac tgt gaa gag ctt tct ttg gat gag ctt gta gcc	1075
Asn Cys Ile Val Asn Cys Glu Glu Leu Ser Leu Asp Glu Leu Val Ala	
310 315 320 325	
atc ctt aca gaa cct aca aat gcg att gtg aaa caa tat atg gag cta	1123
Ile Leu Thr Glu Pro Thr Asn Ala Ile Val Lys Gln Tyr Met Glu Leu	
330 335 340	
ttc gca gaa gaa aac gtc aag tta gtc ttc aaa aaa gaa gcc cta tat	1171
Phe Ala Glu Glu Asn Val Lys Leu Val Phe Lys Lys Glu Ala Leu Tyr	
345 350 355	
gct ata gca aaa aaa gcc aag caa gca aaa act gga gct cgt gct cta	1219
Ala Ile Ala Lys Lys Ala Lys Gln Ala Lys Thr Gly Ala Arg Ala Leu	
360 365 370	

16/111

Figure 6 (Cont.)

```

ggg atg atc cta gaa aat ctc ctt aga gac ctt atg ttt gaa att cct 1267
Gly Met Ile Leu Glu Asn Leu Leu Arg Asp Leu Met Phe Glu Ile Pro
      375                      380                      385

tca gat cct aca gta gaa gct att cat atc caa gaa gac act atc gca 1315
Ser Asp Pro Thr Val Glu Ala Ile His Ile Gln Glu Asp Thr Ile Ala
390                      395                      400                      405

gaa aat aaa gcg cca ata att atc aga agg acc cca gaa gct atc gct 1363
Glu Asn Lys Ala Pro Ile Ile Ile Arg Arg Thr Pro Glu Ala Ile Ala
                        410                      415                      420

tagctctttt tagttcctat tttaggggtg tcatgacaac aattgccata gaagctgcaa 1423

aaaaagttct tatcaaacta cgtaatgcag gatatcaggc ata 1466

```

17/111

**Figure 7: Sequence of *C. pneumoniae* CLP protease subunit gene (SEQ ID NOS: 13 and 14).**

tga	cgt	tag	ac	agc	ctataaaaa	gtctt	agcta	cgtt	ctctagg	gtc	atttcgt	gat	cgggaac	60		
gtat	ggac	ac	aact	gaaaat	tattt	gatga	gga	aacgcaa	atg	aca	ctg	gta	ccc	115		
									Met	Thr	Leu	Val	Pro	5		
tat	ggt	gtc	gag	gat	acg	ggc	cgt	ggt	gaa	agg	gcc	atg	gat	att	tac	163
Tyr	Val	Val	Glu	Asp	Thr	Gly	Arg	Gly	Glu	Arg	Ala	Met	Asp	Ile	Tyr	20
					10				15							
tcc	cgt	ctt	ctg	aaa	gat	cgt	att	gta	atg	atc	ggt	cag	gaa	atc	acg	211
Ser	Arg	Leu	Leu	Lys	Asp	Arg	Ile	Val	Met	Ile	Gly	Gln	Glu	Ile	Thr	35
				25				30								
gag	ccc	ctc	gca	aac	aca	gta	att	gcc	cag	ctc	ctt	ttc	ctc	atg	tcc	259
Glu	Pro	Leu	Ala	Asn	Thr	Val	Ile	Ala	Gln	Leu	Leu	Phe	Leu	Met	Ser	40
							45					50				
gaa	gat	cct	aaa	aag	gat	att	caa	att	ttc	atc	aat	tcc	cca	ggc	ggc	307
Glu	Asp	Pro	Lys	Lys	Asp	Ile	Gln	Ile	Phe	Ile	Asn	Ser	Pro	Gly	Gly	55
						60					65					
tac	atc	acc	gct	gga	ctg	gca	atc	tat	gat	acc	att	cgc	ttt	tta	ggt	355
Tyr	Ile	Thr	Ala	Gly	Leu	Ala	Ile	Tyr	Asp	Thr	Ile	Arg	Phe	Leu	Gly	70
					75					80					85	
tgt	gat	gta	aat	acc	tac	tgc	atc	ggt	caa	gct	gca	tcc	atg	gga	gcc	403
Cys	Asp	Val	Asn	Thr	Tyr	Cys	Ile	Gly	Gln	Ala	Ala	Ser	Met	Gly	Ala	90
				90					95					100		
ctc	tta	tta	tcc	gca	gga	act	aaa	gga	aag	cgt	cac	gct	ctt	ccc	cat	451
Leu	Leu	Leu	Ser	Ala	Gly	Thr	Lys	Gly	Lys	Arg	His	Ala	Leu	Pro	His	105
								110					115			
agc	cgt	atg	atg	atc	cac	caa	cct	tct	gga	ggc	att	atc	gga	aca	tcc	499
Ser	Arg	Met	Met	Ile	His	Gln	Pro	Ser	Gly	Gly	Ile	Ile	Gly	Thr	Ser	120
							125					130				
gca	gac	atc	caa	ctc	caa	gca	gct	gaa	att	cta	aca	cta	aaa	aaa	cac	547
Ala	Asp	Ile	Gln	Leu	Gln	Ala	Ala	Glu	Ile	Leu	Thr	Leu	Lys	Lys	His	135
						140					145					
ctt	gcc	aat	atc	ctc	tct	gaa	tgc	aca	gga	caa	cct	gta	gaa	aaa	att	595
Leu	Ala	Asn	Ile	Leu	Ser	Glu	Cys	Thr	Gly	Gln	Pro	Val	Glu	Lys	Ile	150
					155					160					165	

18/111

Figure 7 (Cont.)

ata gaa gat tct gaa cga gat ttc ttc atg gga gcc gag gaa gcc atc	643
Ile Glu Asp Ser Glu Arg Asp Phe Phe Met Gly Ala Glu Glu Ala Ile	
170 175 180	
tcc tac gga ctt att gat aag gtg gta act tct gcg aaa gaa act aat	691
Ser Tyr Gly Leu Ile Asp Lys Val Val Thr Ser Ala Lys Glu Thr Asn	
185 190 195	
aag gat aca agt agc act tagagagaac atatgaataa aaaaaatcta	739
Lys Asp Thr Ser Ser Thr	
200	
actatttggtt cattttgcgg tcggtctgaa aaagatgtag agaaactgat tgctgggcct	799
tcggtataca ttt	812

19/111

**Figure 8: Sequence of *C. pneumoniae* transglycolase/ transpeptidase gene (SEQ ID NOS: 15 and 16).**

```

gataaaatag aaagacctga tcatttgatg gaaatagcag ctcttcccga ataccaatat 60
ttggaatatc cctcagaaga aagtatcagt cttttatcct atg agc tac cgt aaa 115
                                     Met Ser Tyr Arg Lys
                                     1           5
cgt tcg act cta att gtt cta gga gtg ttt gct ctt tat gct ctt cta 163
Arg Ser Thr Leu Ile Val Leu Gly Val Phe Ala Leu Tyr Ala Leu Leu
                10                15                20
gta ttg cgt tat tat aaa att caa att tgt gaa gga gac cac tgg gcc 211
Val Leu Arg Tyr Tyr Lys Ile Gln Ile Cys Glu Gly Asp His Trp Ala
                25                30                35
gca gaa gct ctc ggg caa cac gaa ttt tgt gtc cgt gat cct ttt cga 259
Ala Glu Ala Leu Gly Gln His Glu Phe Cys Val Arg Asp Pro Phe Arg
                40                45                50
agg ggc acc ttt ttt gct aac acg aca gta cgt aag gga gac aaa gac 307
Arg Gly Thr Phe Phe Ala Asn Thr Thr Val Arg Lys Gly Asp Lys Asp
                55                60                65
ctt cag cag cct ttc gct gtc gat att aca aaa ttt cac ctt tgt gca 355
Leu Gln Gln Pro Phe Ala Val Asp Ile Thr Lys Phe His Leu Cys Ala
                70                75                80                85
gat cct tta gct att ccc gaa tgt cat cgt gat gag atc atc caa ggg 403
Asp Pro Leu Ala Ile Pro Glu Cys His Arg Asp Glu Ile Ile Gln Gly
                90                95                100
att ctc caa ttt att gag ggg cag acc tac gac gac ctc tcc cta aag 451
Ile Leu Gln Phe Ile Glu Gly Gln Thr Tyr Asp Asp Leu Ser Leu Lys
                105                110                115
tta gat aag aaa tct cgg tat tgt aag ctg tat cct tta tta gat gtt 499
Leu Asp Lys Lys Ser Arg Tyr Cys Lys Leu Tyr Pro Leu Leu Asp Val
                120                125                130
tct gtc cat gac cgg cta tcc ctt tgg tgg aaa gga tat gca aca aag 547
Ser Val His Asp Arg Leu Ser Leu Trp Trp Lys Gly Tyr Ala Thr Lys
                135                140                145
cat cgc tta cca aca aac gcc cta ttt ttt att acg gac tac caa cgc 595
His Arg Leu Pro Thr Asn Ala Leu Phe Phe Ile Thr Asp Tyr Gln Arg
                150                155                160                165

```

20/111

Figure 8 (Cont.)

tcg	tat	cct	ttt	ggg	aag	ctc	ctt	gga	caa	gtt	ctc	cat	acc	tta	aga	643
Ser	Tyr	Pro	Phe	Gly	Lys	Leu	Leu	Gly	Gln	Val	Leu	His	Thr	Leu	Arg	
				170					175					180		
gaa	att	aag	gat	gag	aaa	aca	gga	aaa	gcc	ttt	ccc	aca	ggc	ggg	atg	691
Glu	Ile	Lys	Asp	Glu	Lys	Thr	Gly	Lys	Ala	Phe	Pro	Thr	Gly	Gly	Met	
			185					190					195			
gag	gcg	tac	ttt	aat	cat	att	ctg	gaa	ggg	gac	gtt	gga	gag	aga	aag	739
Glu	Ala	Tyr	Phe	Asn	His	Ile	Leu	Glu	Gly	Asp	Val	Gly	Glu	Arg	Lys	
		200					205					210				
ctg	ttg	cgt	tct	cct	ttg	aac	cgt	tta	gat	acg	aat	cgt	gtt	atc	aaa	787
Leu	Leu	Arg	Ser	Pro	Leu	Asn	Arg	Leu	Asp	Thr	Asn	Arg	Val	Ile	Lys	
		215				220					225					
ctg	cct	aaa	gat	ggc	tct	gat	atc	tac	ctt	acg	atc	aat	cct	gtg	atc	835
Leu	Pro	Lys	Asp	Gly	Ser	Asp	Ile	Tyr	Leu	Thr	Ile	Asn	Pro	Val	Ile	
		230			235					240					245	
cag	acc	att	gca	gag	gaa	gaa	ctc	gaa	cgg	ggc	gtg	cta	gaa	gct	aaa	883
Gln	Thr	Ile	Ala	Glu	Glu	Glu	Leu	Glu	Arg	Gly	Val	Leu	Glu	Ala	Lys	
			250						255					260		
gcc	cag	ggg	ggt	agg	ctc	att	cta	atg	aac	tcc	caa	aca	gga	gag	att	931
Ala	Gln	Gly	Arg	Leu	Ile	Leu	Met	Asn	Ser	Gln	Thr	Gly	Glu	Ile		
		265					270						275			
ctt	gca	ctg	gct	caa	tat	ccg	ttt	ttc	gat	ccc	aca	aat	tat	aag	gaa	979
Leu	Ala	Leu	Ala	Gln	Tyr	Pro	Phe	Phe	Asp	Pro	Thr	Asn	Tyr	Lys	Glu	
		280					285					290				
tac	ttc	aat	aac	aaa	gag	cgc	atc	gaa	cat	acg	aag	gta	tct	ttt	gtg	1027
Tyr	Phe	Asn	Asn	Lys	Glu	Arg	Ile	Glu	His	Thr	Lys	Val	Ser	Phe	Val	
		295				300					305					
agc	gat	gtt	ttt	gaa	ccc	ggg	tgc	atc	atg	aaa	cct	ttg	act	gtg	gcg	1075
Ser	Asp	Val	Phe	Glu	Pro	Gly	Ser	Ile	Met	Lys	Pro	Leu	Thr	Val	Ala	
		310			315					320				325		
att	gct	tta	caa	gct	aac	gaa	gag	gct	agc	tta	aaa	tgc	cag	aaa	aag	1123
Ile	Ala	Leu	Gln	Ala	Asn	Glu	Glu	Ala	Ser	Leu	Lys	Ser	Gln	Lys	Lys	
			330					335						340		
att	ttt	gat	cct	gaa	gaa	cct	atc	gat	gtg	acc	agg	aca	ctc	ttc	cct	1171
Ile	Phe	Asp	Pro	Glu	Glu	Pro	Ile	Asp	Val	Thr	Arg	Thr	Leu	Phe	Pro	
			345					350					355			
gga	cga	aaa	gga	tct	ccg	ctt	aag	gat	att	tct	aga	aac	tct	caa	ttg	1219
Gly	Arg	Lys	Gly	Ser	Pro	Leu	Lys	Asp	Ile	Ser	Arg	Asn	Ser	Gln	Leu	
		360					365					370				



21/111

Figure 8 (Cont.)

aat atg tac atg gct atc cag aaa tct tcg aat gtc tat gta gct cag	1267
Asn Met Tyr Met Ala Ile Gln Lys Ser Ser Asn Val Tyr Val Ala Gln	
375 380 385	
ctg gct gac cgc atc ata caa tct tta gga gtg gcc tgg tac caa cag	1315
Leu Ala Asp Arg Ile Ile Gln Ser Leu Gly Val Ala Trp Tyr Gln Gln	
390 395 400 405	
aag ttg cta gct ctg gga ttt gga aga aaa aca ggg atc gag ctt ccc	1363
Lys Leu Leu Ala Leu Gly Phe Gly Arg Lys Thr Gly Ile Glu Leu Pro	
410 415 420	
agt gag gcc tct ggt ttg gtg cct tct ccc cat cgt ttc cat att aat	1411
Ser Glu Ala Ser Gly Leu Val Pro Ser Pro His Arg Phe His Ile Asn	
425 430 435	
ggt tcc ctg gaa tgg tcc tta tct act cca tat tct ttg gct atg gga	1459
Gly Ser Leu Glu Trp Ser Leu Ser Thr Pro Tyr Ser Leu Ala Met Gly	
440 445 450	
tat aat att ttg gca aca ggg ata caa atg gtt caa gcc tac gct atc	1507
Tyr Asn Ile Leu Ala Thr Gly Ile Gln Met Val Gln Ala Tyr Ala Ile	
455 460 465	
ctt gca aac gga ggt tat gcc gtc cgg ccc act tta gta aaa aag atc	1555
Leu Ala Asn Gly Gly Tyr Ala Val Arg Pro Thr Leu Val Lys Lys Ile	
470 475 480 485	
gtc tct gct tca gga gag gaa tat cat ctt cct act aaa gag aag aca	1603
Val Ser Ala Ser Gly Glu Glu Tyr His Leu Pro Thr Lys Glu Lys Thr	
490 495 500	
cga ctc ttt tca gaa gaa att act aga gaa gtt gtt cgt gcc atg cgt	1651
Arg Leu Phe Ser Glu Glu Ile Thr Arg Glu Val Val Arg Ala Met Arg	
505 510 515	
ttt aca acg tta ccc gga ggt tcg gga ttt cga gcc tct cct aag cat	1699
Phe Thr Thr Leu Pro Gly Gly Ser Gly Phe Arg Ala Ser Pro Lys His	
520 525 530	
cac tct agt gct ggg aaa aca gga act aca gaa aag atg att cat gga	1747
His Ser Ser Ala Gly Lys Thr Gly Thr Thr Glu Lys Met Ile His Gly	
535 540 545	
aaa tat gat aaa cgc cgt cat att gct tct ttt ata ggt ttt act ccc	1795
Lys Tyr Asp Lys Arg Arg His Ile Ala Ser Phe Ile Gly Phe Thr Pro	
550 555 560 565	
gta gag agc tcg gag gga aat ttc cca cct tta gtg atg ctc gtc tcc	1843
Val Glu Ser Ser Glu Gly Asn Phe Pro Pro Leu Val Met Leu Val Ser	
570 575 580	

22/111

Figure 8 (Cont.)

ata gat gat cct gaa tat ggt ttg cga gcc gac ggc acg aaa aat tat	1891
Ile Asp Asp Pro Glu Tyr Gly Leu Arg Ala Asp Gly Thr Lys Asn Tyr	
585 590 595	
atg ggg ggg cgt tgt gcg gca ccc att ttt tct agg gtt gct gac cgc	1939
Met Gly Gly Arg Cys Ala Ala Pro Ile Phe Ser Arg Val Ala Asp Arg	
600 605 610	
aca ctc ctc tat tta ggg att ctt cca gac aag aag cta aga aat tgc	1987
Thr Leu Leu Tyr Leu Gly Ile Leu Pro Asp Lys Lys Leu Arg Asn Cys	
615 620 625	
gac gaa gaa gct gct gca tta aag cgt ctc tat gaa gaa tgg aat cgt	2035
Asp Glu Glu Ala Ala Ala Leu Lys Arg Leu Tyr Glu Glu Trp Asn Arg	
630 635 640 645	
tct ccg aaa caa ggg gga acg agg tgaggatctc tatttccatc ttgctataga	2089
Ser Pro Lys Gln Gly Gly Thr Arg	
650	
ctttttaccgt tgagcaaaga ctctctatca gagagcccggt ctctctttta tcctctatga	2149
gtagtttatg tta	2162

23/111

Figure 9: Sequence of *C. pneumoniae* CLPc protease gene (SEQ ID NOS: 17 and 18).

```

gaattttacc aaatttgctg gtttagagcg aagagttgca tcattatattt aaatttcgta 60
tatgcttaag gaaagttcta cccctgtctt ttaggttttt atg ttt gag aag ttc 115
                                     Met Phe Glu Lys Phe
                                     1           5

act aat aga gca aaa caa gtc att aaa ctg gcg aaa aag gag gct cag 163
Thr Asn Arg Ala Lys Gln Val Ile Lys Leu Ala Lys Lys Glu Ala Gln
                        10                      15                      20

cgt tta aat cat aac tac ctg ggt act gag cac atc ctg ctt ggt ctt 211
Arg Leu Asn His Asn Tyr Leu Gly Thr Glu His Ile Leu Leu Gly Leu
                        25                      30                      35

ctc aaa ctt ggt caa ggg gta gct gtt aat gta tta cgc aac ctc ggt 259
Leu Lys Leu Gly Gln Gly Val Ala Val Asn Val Leu Arg Asn Leu Gly
                        40                      45                      50

ata gat ttt gat acg gca cgg caa gag gtg gaa cgc ctg att ggt tat 307
Ile Asp Phe Asp Thr Ala Arg Gln Glu Val Glu Arg Leu Ile Gly Tyr
                        55                      60                      65

ggg cca gaa att caa gtc tac gga gac cct gcc ctt aca gga aga gta 355
Gly Pro Glu Ile Gln Val Tyr Gly Asp Pro Ala Leu Thr Gly Arg Val
                        70                      75                      80                      85

aaa aaa tct ttt gaa tca gca aat gaa gag gcc agc ctt tta gag cac 403
Lys Lys Ser Phe Glu Ser Ala Asn Glu Glu Ala Ser Leu Leu Glu His
                        90                      95                      100

aat tat gtc ggg acg gag cat tta ctc tta ggg atc cta cat caa tca 451
Asn Tyr Val Gly Thr Glu His Leu Leu Leu Gly Ile Leu His Gln Ser
                        105                      110                      115

gat agt gtc gct ctt cag gta tta gaa aac tta cat atc gat cca aga 499
Asp Ser Val Ala Leu Gln Val Leu Glu Asn Leu His Ile Asp Pro Arg
                        120                      125                      130

gag gtt cgt aag gaa att ctt aga gaa tta gag acc ttc aat cta caa 547
Glu Val Arg Lys Glu Ile Leu Arg Glu Leu Glu Thr Phe Asn Leu Gln
                        135                      140                      145

ctt cct cct tcg tcg tcg tct tct tcc tca tcc tct cga agc aac cct 595
Leu Pro Pro Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Arg Ser Asn Pro
                        150                      155                      160                      165

tca tct tca aaa tct cct tta ggt cat agc tta ggt tct gac aaa aac 643
Ser Ser Ser Lys Ser Pro Leu Gly His Ser Leu Gly Ser Asp Lys Asn
                        170                      175                      180

```

24/111

Figure 9 (Cont.)

gaa aag ctt tct gct ctg aaa gca tat ggt tat gat tta acg gag atg	691
Glu Lys Leu Ser Ala Leu Lys Ala Tyr Gly Tyr Asp Leu Thr Glu Met	
185 190 195	
gtc cga gag tct aag ctc gat cct gtc att ggt cgt tct tca gaa gtc	739
Val Arg Glu Ser Lys Leu Asp Pro Val Ile Gly Arg Ser Ser Glu Val	
200 205 210	
gaa cgg ttg att ttg att ctt tgc cga aga aga aaa aac aat cct gta	787
Glu Arg Leu Ile Leu Ile Leu Cys Arg Arg Arg Lys Asn Asn Pro Val	
215 220 225	
ctt att gga gaa gct gga gtt ggt aag act gca att gtt gag ggt ctg	835
Leu Ile Gly Glu Ala Gly Val Gly Lys Thr Ala Ile Val Glu Gly Leu	
230 235 240 245	
gct caa aaa atc att ctg aat gag gtt cct gat gcc tta cgg aaa aag	883
Ala Gln Lys Ile Ile Leu Asn Glu Val Pro Asp Ala Leu Arg Lys Lys	
250 255 260	
cga ctg att act cta gat cta gca tta atg att gct gga aca aaa tat	931
Arg Leu Ile Thr Leu Asp Leu Ala Leu Met Ile Ala Gly Thr Lys Tyr	
265 270 275	
cga ggg caa ttt gag gaa cgg atc aaa gct gtc atg gat gaa gtt cgc	979
Arg Gly Gln Phe Glu Glu Arg Ile Lys Ala Val Met Asp Glu Val Arg	
280 285 290	
aag cat gga aac atc ttg ctc ttc att gac gag ctc cac acg att gta	1027
Lys His Gly Asn Ile Leu Leu Phe Ile Asp Glu Leu His Thr Ile Val	
295 300 305	
gga gca gga gca gct gaa ggt gct atc gat gct tca aac att tta aaa	1075
Gly Ala Gly Ala Ala Glu Gly Ala Ile Asp Ala Ser Asn Ile Leu Lys	
310 315 320 325	
cct gcg tta gcg cga ggt gaa att cag tgt att gga gca act acg ata	1123
Pro Ala Leu Ala Arg Gly Glu Ile Gln Cys Ile Gly Ala Thr Thr Ile	
330 335 340	
gat gag tat cgc aag cac ata gaa aaa gac gca gct tta gaa cgt cgt	1171
Asp Glu Tyr Arg Lys His Ile Glu Lys Asp Ala Ala Leu Glu Arg Arg	
345 350 355	
ttc caa aaa atc gtg gtt cac cct cct agt gta gat gag act att gag	1219
Phe Gln Lys Ile Val Val His Pro Pro Ser Val Asp Glu Thr Ile Glu	
360 365 370	
att tta cgt ggc ctc aag aaa aag tat gaa gaa cat cac aat gtc ttc	1267
Ile Leu Arg Gly Leu Lys Lys Lys Tyr Glu Glu His His Asn Val Phe	
375 380 385	

25/111

Figure 9 (Cont.)

att act gaa gaa gct tta aaa gca gct gcg act ctt tct gat caa tat	1315
Ile Thr Glu Glu Ala Leu Lys Ala Ala Ala Thr Leu Ser Asp Gln Tyr	
390 395 400 405	
ggt cat gga cgt ttc ctc cct gat aaa gca ata gat ctt tta gat gaa	1363
Val His Gly Arg Phe Leu Pro Asp Lys Ala Ile Asp Leu Leu Asp Glu	
410 415 420	
gct ggg gct cgt gtc cgt gtg aat aca atg ggt cag cct aca gat tta	1411
Ala Gly Ala Arg Val Arg Val Asn Thr Met Gly Gln Pro Thr Asp Leu	
425 430 435	
atg aag cta gag gct gaa atc gaa aat aca aaa ttg gcc aaa gag cag	1459
Met Lys Leu Glu Ala Glu Ile Glu Asn Thr Lys Leu Ala Lys Glu Gln	
440 445 450	
gcc att gga act caa gaa tac gaa aaa gct gca ggt tta cgt gat gaa	1507
Ala Ile Gly Thr Gln Glu Tyr Glu Lys Ala Ala Gly Leu Arg Asp Glu	
455 460 465	
gag aaa aaa ctt cgc gaa cgt ctg caa agt atg aaa cag gaa tgg gaa	1555
Glu Lys Lys Leu Arg Glu Arg Leu Gln Ser Met Lys Gln Glu Trp Glu	
470 475 480 485	
aat cat aaa gaa gag cac caa gtt cct gta gat gaa gaa gca gtc gct	1603
Asn His Lys Glu Glu His Gln Val Pro Val Asp Glu Glu Ala Val Ala	
490 495 500	
cag gta gtt tct cta caa aca gga att ccc tca gca agg ctc aca gaa	1651
Gln Val Val Ser Leu Gln Thr Gly Ile Pro Ser Ala Arg Leu Thr Glu	
505 510 515	
gct gaa agt gag aag ctt ctg aag tta gaa gac acg tta aga aga aaa	1699
Ala Glu Ser Glu Lys Leu Leu Lys Leu Glu Asp Thr Leu Arg Arg Lys	
520 525 530	
gtc att ggt caa aat gat gcc gtt acc agc att tgc cgt gcc atc cga	1747
Val Ile Gly Gln Asn Asp Ala Val Thr Ser Ile Cys Arg Ala Ile Arg	
535 540 545	
cgt tct cga aca ggg atc aaa gat cct aac cga cct acg ggc tcc ttc	1795
Arg Ser Arg Thr Gly Ile Lys Asp Pro Asn Arg Pro Thr Gly Ser Phe	
550 555 560 565	
cta ttc ctt ggg cct acc ggt gta ggg aaa agc ctg ctc gcc caa caa	1843
Leu Phe Leu Gly Pro Thr Gly Val Gly Lys Ser Leu Leu Ala Gln Gln	
570 575 580	
att gct ata gag atg ttc ggt ggt gaa gac gct ctg att cag gta gac	1891
Ile Ala Ile Glu Met Phe Gly Gly Glu Asp Ala Leu Ile Gln Val Asp	
585 590 595	

26/111

Figure 9 (Cont.)

atg tca gag tac atg gag aaa ttt gct gct acc aag atg atg gga tca	1939
Met Ser Glu Tyr Met Glu Lys Phe Ala Ala Thr Lys Met Met Gly Ser	
600 605 610	
cct cca gga tat gta ggt cat gaa gaa ggg ggc cac ctt acg gaa cag	1987
Pro Pro Gly Tyr Val Gly His Glu Glu Gly Gly His Leu Thr Glu Gln	
615 620 625	
gta cgt cgc cgt cct tac tgc gtt gtt ctc ttt gat gag ata gaa aag	2035
Val Arg Arg Arg Pro Tyr Cys Val Val Leu Phe Asp Glu Ile Glu Lys	
630 635 640 645	
gca cac cca gac att atg gac ctg atg ttg caa att tta gag caa gga	2083
Ala His Pro Asp Ile Met Asp Leu Met Leu Gln Ile Leu Glu Gln Gly	
650 655 660	
cgt ctt act gat tct ttt ggt cgc aaa gtg gat ttc cgt cat gcc att	2131
Arg Leu Thr Asp Ser Phe Gly Arg Lys Val Asp Phe Arg His Ala Ile	
665 670 675	
att atc atg acc tcc aat ttg gga gct gat ctc att cgt aaa agc gga	2179
Ile Ile Met Thr Ser Asn Leu Gly Ala Asp Leu Ile Arg Lys Ser Gly	
680 685 690	
gaa att ggt ttt ggc ttg aag tcc cat atg gac tat aag gtc atc caa	2227
Glu Ile Gly Phe Gly Leu Lys Ser His Met Asp Tyr Lys Val Ile Gln	
695 700 705	
gag aaa atc gaa cat gct atg aag aaa cac tta aag cct gag ttc att	2275
Glu Lys Ile Glu His Ala Met Lys Lys His Leu Lys Pro Glu Phe Ile	
710 715 720 725	
aac cgt ttg gat gaa agt gtg att ttc cgt ccc ctc gag aaa gaa tct	2323
Asn Arg Leu Asp Glu Ser Val Ile Phe Arg Pro Leu Glu Lys Glu Ser	
730 735 740	
cta tcg gag atc atc cat tta gag atc aac aaa ctg gac tcg aga ctg	2371
Leu Ser Glu Ile Ile His Leu Glu Ile Asn Lys Leu Asp Ser Arg Leu	
745 750 755	
aaa aac tac caa atg gct ttg aac atc cca gac tct gtg att tcc ttc	2419
Lys Asn Tyr Gln Met Ala Leu Asn Ile Pro Asp Ser Val Ile Ser Phe	
760 765 770	
cta gta acg aag ggg cat tct cca gaa atg gga gca cgt cct cta cgc	2467
Leu Val Thr Lys Gly His Ser Pro Glu Met Gly Ala Arg Pro Leu Arg	
775 780 785	
cgt gtc att gag cag tac ctt gaa gat cct cta gcg gag ctc ttg ctt	2515
Arg Val Ile Glu Gln Tyr Leu Glu Asp Pro Leu Ala Glu Leu Leu Leu	
790 795 800 805	

27/111

Figure 9 (Cont.)

```

aaa gag tcc tgc cgt caa gaa gct cgc aag cta cga gca acc ttg gtt 2563
Lys Glu Ser Cys Arg Gln Glu Ala Arg Lys Leu Arg Ala Thr Leu Val
                        810                        815                        820

gaa aat cgc gtt gcc ttt gaa agg gaa gaa gag gag cag gaa gct gct 2611
Glu Asn Arg Val Ala Phe Glu Arg Glu Glu Glu Glu Gln Glu Ala Ala
                        825                        830                        835

ctc cct agc cct cac ttg gaa tca taggaacgtc gataactcca ctaccaaggc 2665
Leu Pro Ser Pro His Leu Glu Ser
                        840                        845

aggtatctcc ttgataaaac gctattgttt gtcctggagt taccgccttg acgggttgtg 2725

aaaatcgcac ctt 2738

```

28/111

Figure 10: Sequence of *C. pneumoniae* Thioredoxin gene (SEQ ID NOS: 19 and 20).

```

gattcaggtt ctagtgagct tatgctcatg gaagttcaag tcttcttagc tgcaagaaaa 60
taacagggac agtaattcga tttttcgaga agggaaactt atg gta aag atc ata 115
                                     Met Val Lys Ile Ile
                                     1 5

tca agt gaa aat ttt gac tct ttt att gca tcg ggg ctc gtt ctc gtt 163
Ser Ser Glu Asn Phe Asp Ser Phe Ile Ala Ser Gly Leu Val Leu Val
          10          15          20

gat ttc ttt gca gaa tgg tgt ggc ccc tgt cgg atg ctc act cct atc 211
Asp Phe Phe Ala Glu Trp Cys Gly Pro Cys Arg Met Leu Thr Pro Ile
          25          30          35

tta gaa aat ctt gct gcg gaa ctt cct cat gtc act att gga aaa atc 259
Leu Glu Asn Leu Ala Ala Glu Leu Pro His Val Thr Ile Gly Lys Ile
          40          45          50

aat ata gat gag aac agc aag cct gca gaa acg tac gaa gtc agc tct 307
Asn Ile Asp Glu Asn Ser Lys Pro Ala Glu Thr Tyr Glu Val Ser Ser
          55          60          65

att cct acg ctt att ctt ttt aag gat ggg aac gag gtg gct cgg gtc 355
Ile Pro Thr Leu Ile Leu Phe Lys Asp Gly Asn Glu Val Ala Arg Val
          70          75          80          85

gta ggt ctt aag gat aaa gaa ttc cta acc aat ctt atc aat aag cac 403
Val Gly Leu Lys Asp Lys Glu Phe Leu Thr Asn Leu Ile Asn Lys His
          90          95          100

gct taaaaagacg ctgcaatatt aaaccgtagg attctttttgc aatgctacgg 456
Ala

ttttctgcct taccacttca tataaaaacga tcctacact ggtagctaaa ttt 509

```



Figure 11. Restriction enzyme analysis of the *C. pneumoniae* ATP-binding cassette gene (SEQ ID NO: 1).

BbsI  
 BsaJI  
 MboII  
 TaqI  
 BstDSI  
 Hpy188IX  
 MnlI  
 BccI  
 PleI  
 HinfI  
 NlaIII  
 1  
 AATCTCATTCCCCATCGACTAAATCCACCACGGACTCCGACCTCCCATGTCTTCAATCC  
 TTAGAGTAAGGGGGTAGCTGATTTAGGTGGTGCCTGAGGCTGGAGGGTACAGAAGTTAGG  
 60  
 MseI  
 SfaNI  
 CviJI  
 RsaI  
 MboII  
 ScaI  
 NsiI  
 CviRI  
 MmeI  
 MaeII  
 SspI  
 Tsp509I  
 TatI  
 61  
 ATATGAACGTAATATTAAGTAGCAAATTGAGTACTATATAATGAAGATGCATAGGCTTAA  
 TATACTTGCATTATAATTCATCGTTTAACTCATGATATATTACTTCTACGTATCCGAATT  
 120  
 HaeIV  
 Hin4I  
 DpnI  
 MboII  
 Fnu4HI  
 Hpy188IX  
 AluI  
 Sau3AI  
 CviJI  
 TseI  
 BbvI  
 121  
 ACCTACCTTAAAAAGTCTGATCCCTAATCTTCTTTTCTTATTGCTCACTCTTTCAAGCTG  
 TGGATGGAATTTTTCAGACTAGGGATTAGAAGAAAAGAATAACGAGTGAGAAAGTTCGAC  
 180  
 DpnI  
 NlaIII  
 Sau3AI  
 Bsu36I  
 Hin4I  
 DdeI  
 CviJI  
 181  
 CTCAAAGCAAAAACAAGAACCCTTAGGAAAACATCTCGTTATTGCGATGAGCCATGATCT  
 GAGTTTCGTTTTTGTICTTGGGAATCCTTTTGTAGAGCAATAACGCTACTCGGTACTAGA  
 240

30/111

Figure 11 (Cont.)

```

          DpnI
        BstYI |
        Sau3AI |
        BfaI | |
        AlwI | | |
          | | | |
CGCCGACCTAGATCCTCGCAATGCCTATTTAAGCAGAGATGCTTCCCTAGCAAAAGCCCT
241 -----+-----+-----+-----+-----+-----+-----+ 300
GCGGCTGGATCTAGGAGCGTTACGGATAAATTTCGTCTCTACGAAGGGATCGTTTTCGGGA

          DpnI
        BclI |
        Sau3AI | HinfI
        MnlI | | TfiI
          | | | |
CTATGAAGGACTGACAAGAGAACTGATCAAGGAATCGCACTGGCTCTTGCAGAAAGTTA
301 -----+-----+-----+-----+-----+-----+-----+ 360
GATACTTCCTGACTGTTCTCTTTGACTAGTTCCTTAGCGTGACCGAGAACGTCTTTCAAT

          Hpy188IX
          DpnI
        Sau3AI |
          | |
TACCCTGTCAAAAGATCATAAGGTCTATACCTTTAAACTCAGACCTTCTGTGTGGAGCGA
361 -----+-----+-----+-----+-----+-----+-----+ 420
ATGGGACAGT'TTTCTAGTATTCCAGATATGGAAATTTGAGTCTGGAAGACACACCTCGCT

          ApoI
          Tsp509I
          RsaI HphI |
        Bst4CI |NspV | |
        TatI |TaqI | |
        BccI |
          | |
TGGCACTCCACTCACTGCTTATGACTTTGAAAAATCTATAAAACAACGTACTTCAAGA
421 -----+-----+-----+-----+-----+-----+-----+ 480
ACCGTGAGGTGAGTGACGAATACTGAAACTTTTATAGATATTTTGTGACATGAAGCTTCT

          ApoI
          Tsp509I
        MboII |
        MseI |
          | |
ATTTTACCTTCCATACATACTTTACTCGGCGTGATTAAAAATCTTCGGCAATCCACAA
481 -----+-----+-----+-----+-----+-----+-----+ 540
TAAAAGTGGAAGGTATGTATGAAATGAGCCGCACTAATTTTAAAGAAGCCGTTAGGTGTT

          DpnI
        Hpy178III BciVI
          | |
        Sau3AI |
          | |
TGCTCAAAAATCTCTGGAACTCTTGGGATACAGGCAAAAGATGATCTTACTTTGGTGAT
541 -----+-----+-----+-----+-----+-----+-----+ 600
ACGAGTTTTTAGAGACCTTTGAGAACCCTATGTCCGTTTTCTACTAGAATGAAACCACTA

```

31/111

Figure 11 (Cont.)

```

                                Sth132I
                                BscGI
                                CjePI
                                Cac8I
                                |
                                |
                                |
HphI
BfaI |CjePI
| | |
TACCCTAGAGCAACCTTTCCCATACTTTCTCACACTTATCGCTCGCCCCGTATTCTCCCC
601 -----+-----+-----+-----+-----+-----+ 660
ATGGGATCTCGTTGGAAGGGTATGAAAGAGTGTGAATAGCGAGCGGGGCATAAGAGGGG

                                Bsu36I HinfI
                                DdeI TfiI
                                FokI
                                BccI
                                |
                                |
                                |
TGTTCATCACACCCTTAGGGAATCCTATAAGAAAGGAACACCCCATCCACATACATCTC
661 -----+-----+-----+-----+-----+-----+ 720
ACAAGTAGTGTGGGAATCCCTTAGGATATTCTTTCCTTGTGGGGGTAGGTGTATGTAGAG

                                ApaI
                                BanII
                                BseSI
                                Bsp1286I
                                BmgI
                                CviJI
                                HaeIII
                                NlaIV
                                EcoO109I
                                Sau96I
                                Sau96I
                                MseI
                                NlaIII
                                Tsp509I
                                MseI
                                ||
                                ||
CAATGGGCCCTTTGTCTTAAAAAACATGAACACCAAACTACTTAATTTTAGAAAAAAA
721 -----+-----+-----+-----+-----+-----+ 780
GTTACCCGGGAAACAGAATTTTTTTGTACTTGTGGTTTTGATGAATTAATCTTTTTTT

                                HinfI
                                NlaIII
                                TfiI
                                HaeIV
                                Hin4I
                                Hpy178III
                                RcaI
                                DpnI
                                BclI
                                Sau3AI
                                MnlI
                                MslI
                                HaeIII
                                Tsp45I
                                HinfI
                                Tth111I
                                HphI
                                MaeIII
                                Tsp509I
                                TaqII
                                MseI
                                PleI
                                |
                                |
                                |
TCCTCACTACTATGATCATGAATCAGTAAAGTTAGACCGAGTCACCTTAAAAATTATCCC
781 -----+-----+-----+-----+-----+-----+ 840
AGGAGTGATGATACTAGTACTTAGTCATTTCAATCTGGCTCAGTGGAAATTTTAATAGGG

```

32/111

Figure 11 (Cont.)

```

                MnlI
              CviJI |
            HgaI | |
      BsaHI  MwoI | |   XmnI           SfcI           HphI CviJI BsaJI StyI
            |   | |   |           |           |           |   |
841  -----+-----+-----+-----+-----+-----+-----+-----+-----+ 900
      AGACGCCTCCACAGCCACGAAACTTTTCAAAAGTAAATCTATAGATTGGATTGGCTCACC
      TCTGCGGAGGTGTCGGTGCTTTGAAAAGTTTTTCATTTAGATATCTAACCTAACCGAGTGG

                EcoRV
            Hpy188IX |
            HaeII | |
            HhaI | | |
      Eco47III | | | |           MboII           HinfI
            | | | |           BbsI |           TfiI
            | | | |           |           XmnI |
            | | | |           |           |
901  TTGGAGCGCTCCGATATCTAACGAAGACCAAAAAGTTCTCTCCCAAGAAAAGATTCTTAC
      -----+-----+-----+-----+-----+-----+-----+-----+ 960
      AACCTCGCGAGGCTATAGATTGCTTCTGGTTTTTCAAGAGAGGGTTCTTTTCTAAGAATG

                                BspMI
                            Tth111II   CviRI |           MnlI
                                |         |         |
961  CTATTCTGTTTCAAGCACCACCCTTCTTATCTATAACCTGCAAAAACCTCTAATACAAA
      -----+-----+-----+-----+-----+-----+-----+-----+ 1020
      GATAAGACAAAGTTCGTGGTGGGAAGAATAGATATTGGACGTTTTTGGAGATTATGTTTT

                                BssSI
                                HinfI |
                                MseI | |
            Hpy178III   BseMII   AflII | | |
            Bsu36I |   BsrDI |   SmlI | | |
            DdeI |   CviJI |   HaeIV   Eco57I | | |
      CviJI | |   MnlI | |   NlaIII   Hin4I   PleI | | |
            | | |   | | |   |         |         | | |
1021  TAAAGCCCTCAGGAAAGCCATTGCTCATGCTATTGATAGAAAATCTATCTTAAGACTCGT
      -----+-----+-----+-----+-----+-----+-----+-----+ 1080
      ATTCGGGAGTCCTTTTCGGTAACGAGTACGATAACTATCTTTTAGATAGAATTCTGAGCA

                MaeIII
              AluI |
      Hpy178III   CviJI |   BfaI           MboII
            |         | |         |
1081  GCCTTCAGGACAAGAAGCTGTAACCTAGTTCCCCCAAATCTTTCACAACTCAATCTTCA
      -----+-----+-----+-----+-----+-----+-----+-----+ 1140
      CGGAAGTCCTGTTCTTCGACATTGAGATCAAGGGGGTTTAGAAAAGTGTGAGTTAGAAGT

```

33/111

Figure 11 (Cont.)

```

      DpnI
      BglII |
      BstYI |
      Sau3AI |
      | |
      AAAAGAGATCTCAACAGAAGAACGACAAACAAAAGCCAGAGCATATTTTCAAGAAGCTAA
1141 -----+-----+-----+-----+-----+-----+-----+ 1200
      TTTTCTCTAGAGTTGTCTTCTTGCTGTTTGTTCGGTCTCGTATAAAAGTTCTTCGATT

                                     HinfI
                                     TfiI
                                     MnlI |
                                     SfcI | |
                                     AloI   BseMII | | |
                                     DdeI |   SfaNI | | | | TaqI
      Hpy188IX   FokI   | | |
      | | |
      AGAAACACTTTCTGAAAAGAACTCGCAGAACTCAGCATCCTCTATCCTATAGATTCTCTC
1201 -----+-----+-----+-----+-----+-----+-----+ 1260
      TCTTTGTGAAAGACTTTTTCTTGAGCGTCTTGAGTCGTAGGAGATAGGATATCTAAGGAG

      Bce83I   Hpy178III
      ApoI |   SmlI |
      CjePI |   AluI | |
      EcoRI |   BccI   CviJI | |
      Tsp509I |MnlI |   MnlI | | |   CjePI   MseI   Bsu36I   HaeIV
      | | |   | | | | |   | | |   | | |   DdeI   Hin4I
      | | |   | | | | |   | | |   | | |   | | |
      GAATTCCTCCATCATAGCTCAAGAAATCCAAAGACAACCTTAAAGATACCTTAGGATTGAA
1261 -----+-----+-----+-----+-----+-----+-----+ 1320
      CTTAAGGAGGTAGTATCGAGTTCTTTAGGTTTCTGTTGAATTTCTATGGAATCCTAACTT

                                     DraI
                                     MseI |
      BsaJI   BslI |   TspRI | |
      StyI   PflMI |RsaI   BtsI | | |   MaeII   MboII
      | | |   | | | | |   | | |   | | |
      AATCAAAATCCAAGGCATGGAGTACCACTGCTTTTTTAAAGAAACGTCGTCAAGGAGATTT
1321 -----+-----+-----+-----+-----+-----+-----+ 1380
      TTAGTTTTAGGTTCCGTACCTCATGGTGACGAAAAATTTCTTTGCAGCAGTTCTCTAA

                                     BsaAI
                                     SnaBI
                                     MaeII |   Sth132I
      MnlI   BccI   AciI | | |CviJI |CviJI |
      | | |   | | | | |   | | |   | | |
      CTTCATAGCGACAGGAGGATGGATTGCGGAATACGTAAGCCCCGTAGCCTTCCTATCTAT
1381 -----+-----+-----+-----+-----+-----+-----+ 1440
      GAAGTATCGCTGTCCTCCTACCTAACGCCTTATGCATTGGGGCATCGGAAGGATAGATA

```

Figure 11 (Cont.)

BsaI BsmAI MnlI BsaXI |TspRI  
 TCTAGGCAACCCCAGAGACCTCACACAATGGAGAAACAGTGATTACGAAAAGACTTTAGA  
 1441 -----+-----+-----+-----+-----+-----+-----+ 1500  
 AGATCCGTTGGGGTCTCTGGAGTGTGTTACCTCTTTGTCTACTAATGCTTTTCTGAAATCT  
  
 DraI  
 MseI |  
 MnlI ApoI | | HhaI  
 BsaXI NlaIII |Tsp509I | | ThaI |  
 GAAACTCTATCTCCCTCATGCCTACAAAGAGAATTTAAACGCGCAGAAATGATAATAGA  
 1501 -----+-----+-----+-----+-----+-----+-----+ 1560  
 CTTTGAGATAGAGGGAGTACGGATGTTTCTCTTAAATTTTGC GCGTCTTTACTATTATCT  
  
 Sth132I  
 MboII |  
 MboII | | FokI BceFI  
 AGAAGAAACCCCGATTATCCCCCTGTATCACGGCAAATATATTTACGCTATACATCCTAA  
 1561 -----+-----+-----+-----+-----+-----+-----+ 1620  
 TCTTCTTTGGGGCTAATAGGGGGACATAGTGCCGTTTATATAAATGCGATATGTAGGATT  
  
 MseI  
 DpnI CviJI AflIII |  
 BstYI | HaeI CjePI |  
 Hpy188IX | HaeIII DpnI SmlI |  
 Sau3AI | EarI | BglII | EcoRV |  
 MboII | | BfaI | | BstYI | ClaI | |  
 Hpy178III XmnI | | AlwI | | Sau3AI | TaqI | |  
 AATCCAGAATACATTCCGATCTCTTCTAGGCCACACAGATCTCAAAAATATCGATATCTT  
 1621 -----+-----+-----+-----+-----+-----+-----+ 1680  
 TTAGGTCTTATGTAAGCCTAGAGAAGATCCGGTGTGTCTAGAGTTTTTATAGCTATAGAA  
  
 Hpy188IX CjePI  
 DpnI | ApoI |  
 BstYI | | Tsp509I |  
 Sau3AI | | MseI | | MseI  
 AlwI | | | Tsp509I | | Hpy178III Tsp509I |  
 AAGTTAGATCCGAAATGGAAAAATTAAAAATTTTATAGACAATCTTGAAAAGAGAATTAA  
 1681 -----+-----+-----+-----+-----+-----+-----+ 1740  
 TTCAATCTAGGCTTTACCTTTTTTAATTTTAAAAATAICTGTAGAACTTTTCTCTTAATT

35/111

Figure 11 (Cont.)

```

          Tsp509I
        Tsp509I DraI|      MunI
      ApcI      | SwaI|      Tsp509I
Tsp509I  MseI|MseI||      CviRI|      DdeI
      |      ||  ||      ||      |
      AAATTTTAAATTTAAATTATAGTTGCAATTGAAAACGCCCTAAGAA
1741  -----+-----+-----+-----+----- 1787
      TTTAAAAATTAAATTTAATATCAACGTTAACTTTGCGGGGATTCTT

```

36/111

**Figure 12. Restriction enzyme analysis of the *C. pneumoniae* secretory locus protein gene (SEQ ID NO: 3).**

```

          Hpy178III
            DpnI |
          Sau3AI | |
        Hpy178III | | | Hpy178III MunI Sth132I
Hpy178III AlwI | | | | XmnI |Tsp509I MseI | BscGI
| | | | | | | | | | | | | |
1  TTCCAGAGAAATCCTGATCCTGAAAACTTCCTGAAACAATTGCTTTAACTATAACACGG
   -----+-----+-----+-----+-----+-----+-----+ 60
   AAGGTCTCTTTAGGACTAGGACTTTTTGAAGGACTTTGTAAACGAAATTGATATTGTGCC

                                HincII
                                HpaI
                                MjaIV
                                MseI | AciI
                                BsaJI MnlI | | XcmI
NlaIV          StyI MaeII | | Tsp509I BslI | CviJI
| | | | | | | | | | | | | |
61 GAACCTAAAGCATATCCTCCAAGGACGTTAACATACCAATTGCGGTTGGGAAATAAGCC
   -----+-----+-----+-----+-----+-----+-----+ 120
   CTTGGATTTCGTATAGGAGGTTCTGCAATTGTATGGTTAAACGCCAACCTTTATTCGG

                                BbvI
                                SfaNI
CviRI          Tth111III Bst4CI
| | | | | | | | | | | | | |
121 TATGCAACCTTTTATCTTTACTTTACTGTGCTTGACATCTTTGGTTTCTTTAGTCGCCTT
   -----+-----+-----+-----+-----+-----+-----+ 180
   ATACGTTGGAAAATAGAAATGAAATGACACGAACTGTAGAAACCAAAGAAATCAGCGGAA

                                AclI
Fnu4HI          MaeII
TseI | MjaIV | BsiHKAI
MwoI | | MwoI BsmI | | Bsp1286I SfcI MaeII
| | | | | | | | | | | | | |
181 TGATGCTGCGAATGCTCGTAAACGTTGTGCCTGTGCTCAAACATAGAACGTGGAGAGAA
   -----+-----+-----+-----+-----+-----+-----+ 240
   ACTACGACGCTTACGAGCATTTGCAACACGGACACGAGTTTGATATCTTGCACCTCTCTT

                                Hpy178III
AloI Tth111III          TaqI |
| | | | | | | | | | | | | |
241 CTTCTTTTCCATAAAACGCTCTGCTTGTGCTGAAATCGAATATCAAGAAAAATCTCGCCA
   -----+-----+-----+-----+-----+-----+-----+ 300
   GAAGAAAAGGTATTTTGCAGACGAACACGACTTTAGCTTATAGTTCTTTTATAGACGGT

```



37/111

Figure 12 (Cont.)

```

      MunI
      Tsp509I
      BbvCI | BseMII
      Bpu10I | HinfI
      DdeI | MnlI TfiI
      | | | |
      CGCCTCAGCAATTGAAAGAAATCTCAAAGATAAAGGCAAAGTCACTCCAAAGCAGATTGC
301 -----+-----+-----+-----+-----+-----+-----+ 360
      GCGGAGTCGTAACTTCTTAGAGTTTCTATTTCCGTTTCAGTGAGGTTTCGTCTAACG

      CviJI
      HaeI
      HaeIII
      AluI
      CviJI
      MwoI | DdeI
      | | |
      Bst4CI
      BspMI |
      NlaIV
      CviRI |
      Bce83I |
      | |
      GAAAGTAGCTACTAAGAAAAAGCAAAGATACCGTTTATTGCAGGTTCCTTTTCAAGGCC
361 -----+-----+-----+-----+-----+-----+-----+ 420
      CTTTCATCGATGATTCTTTTTCGTTTCTATGGCAAATAACGTCCAAGGAAAAAGTTCCGG

      BsmI
      SfcI |
      SmlI
      Hpy188IX MnlI |
      | |
      DdeI Hpy178III MnlI | |
      MnlI | MjaIV | Sth132I | |
      | | | |
      TCCGAATAACTCAAGGTATAACCTCTATGCTTTGCTTAGTGAACCTCCCGAATGCTATAG
421 -----+-----+-----+-----+-----+-----+-----+ 480
      AGGCTTATTGAGTTCCATATTGGAGATACGAAACGAATCACTTGGAGGGCTTACGATATC

      BtrI
      MjaIV
      HaeIV SfaNI
      Hin4I NlaIII |
      | |
      MaeIII
      MaeII |
      TaqI | | Sth132I | |
      | | | |
      CGATACAGCATCATGGTATGCTATTTTATTCGGTTACTTCGACGTGCTTATGTAGACAC
481 -----+-----+-----+-----+-----+-----+-----+ 540
      GCTATGTCGTAGTACCATACGATAAAAAATAAGCCAATGAAGCTGCACGAATACATCTGTG

      AlwI
      Hpy188IX |
      DdeI | |
      MnlI | |
      DpnI | | |
      BstYI | | |
      Sau3AI | | |
      ScrFI | | | |
      EcoRII | | | |
      BseMII | | | |
      BscGI RsaI | | | | | BccI
      | | | | |
      GGGAAATGTACCTCCTGGATCTGAGTATGCCATCGCTAATGCTTTGATAAGTAACAAACA
541 -----+-----+-----+-----+-----+-----+-----+ 600
      CCCTTTACATGGAGGACCTAGACTCATACGGTAGCGATTACGAACTATTCATTGTTTGT

```

Figure 12 (Cont.)

[illegible]

39/111

Figure 12 (Cont.)

```

                                Sth132I
                                MslI
                                Hpy178III|
                                DpnI
                                Sau3AI |
                                SfaNI |
                                BfaI |
DpnI
NlaIV
BamHI |
BstYI |
NlaIII |
Sau3AI |
                                Hpy178III |
                                XmnI
                                AluI
                                CviJI
                                Bst4CI
                                AlwI
                                FokI
                                XbaI
                                MaeII
CATGGATCCCCTACTGTTAGAGCTGTTCTAGATCATCCCGATGCTTATAGGGAAACGTC
781 -----+-----+-----+-----+-----+-----+-----+ 840
GTACCTAGGGGATGACAATCTTCGACAAGATCTAGTAGGGCTACGAATATCCCTTTGCAG

                                HphI
                                BccI
                                HhaI
                                CjePI
                                BccI
                                HhaI
                                AcI
                                CjePI
                                HpaI
                                FokI
                                NlaIII
                                NspI
                                BstXI
                                BbvI
GCTCCTGCGCGATGGCATTGGAAGCGGTGAAGCGTCAAGAACATGCCATCCAAGAACA
841 -----+-----+-----+-----+-----+-----+-----+ 900
CGAGGACGCGCTACCGTAAACCCTTCGCCACTTCGCAGTTCTTGACGGTAGGTTCTTGT

Fnu4HI
AluI
CviJI
MspA1I
PvuII
TseI
Fnu4HI
TseI
ScrFI
CviJI
EcoRII
HaeI
HaeIII
MscI
NlaIII
EaeI
                                AluI
                                CviJI
                                DraI
                                BbvI
                                MseI
                                EciI
                                BbvI
                                ScrFI
                                AluI
                                SfaNI
                                Fnu4HI
                                CviJI
                                TseI
TGGCCAGGCAGCTGCTTTGGAGCTTTTAAACACGCACCGACTTCCGCCTGGAGCTGCG
901 -----+-----+-----+-----+-----+-----+-----+ 960
ACCGGTCCGTGACGAAACCTCGAAAAATTTGTGCGTGGCTGAAGGCGGACCTCGACGC

```

40/111

Figure 12 (Cont.)

```

                MaeIII
                BpmI|
                CviRI||      DdeI  TaqI                      MseI
                |||          |    |                          |
AGATAAGATGCAGTTACTTCTAAGTCGATACGATTGCTCCCCTTATTAAATAAAAAAAT
961 -----+-----+-----+-----+-----+-----+-----+ 1020
TCTATTCTACGTCAATGAAGATTCAGCTATGCTAAACGAGGGGAATAATTTATTTTTTTTA

                MjaIV
                SimI      BcgI
                AccI|      DdeI  |
                ||          |    |
GTTTCGACTACACCTTAGGAAGTGCCGGAGATTACTTATTTTTGGTAGACCCAGATACTAA
1021 -----+-----+-----+-----+-----+-----+-----+ 1080
CAAGCTGATGTGGAATCCTTCACGGCCTCTAATGAATAAAAACCATCTGGGTCTATGATT

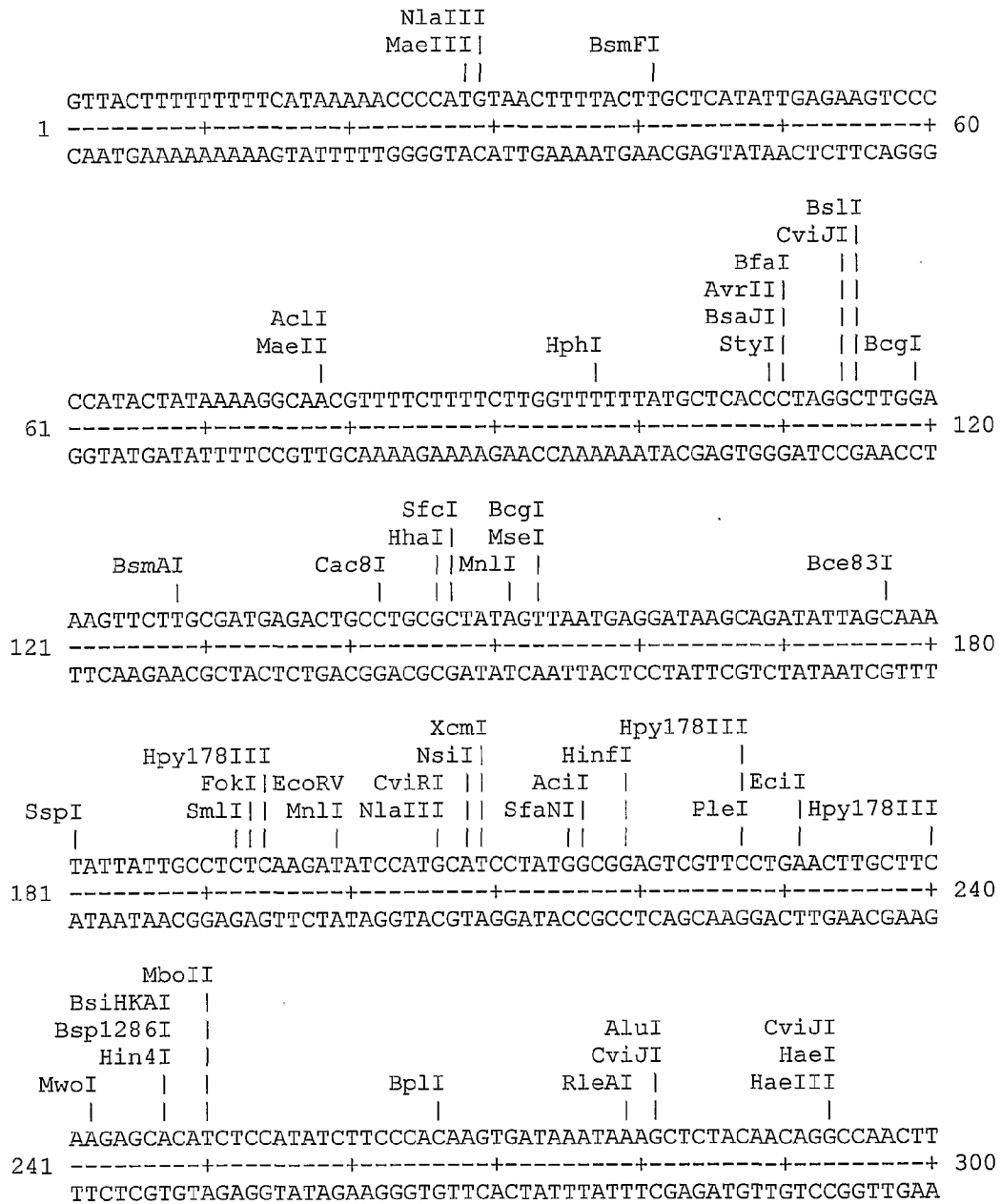
                Tsp509I
                Tsp509I  |
                Tsp509I  |    |
                Hpy178III|      Tsp509I  |    |      SspI
                BbvI  ||      Fnu4HI      MseI  |    |      BcgI  ||  PsiI|MseI| MseI  |
Tsp509I |    ||      TseI|      BcgI  ||  ||  ||  ||  ||  ||  ||  ||
|  |  ||      ||      |  |  |  |  |  |  |  |  |  |  |  |  |
GGCAATTTCTCGATGTCGCTGCCCTTCAAAGAGTATTAAATTATAATTTAATTTAATAT
1081 -----+-----+-----+-----+-----+-----+-----+ 1140
CCGTTAAAGAGCTACAGCGACGGGAAGTTCTCATAATTTAATATTAAATTAAAATTATA

                RsaI
                ScaI
                DraI      Tsp509I  MseI  TatI  |      SspI  SfcI
                MseI|      |    |  |    |      |    |
                ||          |    |  |    |      |    |
TTATTTTAAATAGTTTTTTTTTIGATAATTGTCTTAATAAGTACTATAAAAAATATTTCTAT
1141 -----+-----+-----+-----+-----+-----+-----+ 1200
AATAAAATTTATCAAAAAAACTATTAACAGAATTATTCATGATATTTTTTATAAAGATA

                BsaI
                BsmAI
                NlaIII|
                BsaJI  ||
                BstDSI  ||
                NcoI    ||
                StyI    ||
                AvaII  |  ||
                Sau96I  |  ||      SimI
                |  |  ||      |
AGGTAGGACCATGGCAGACGAGACCC
1201 -----+-----+-----+-----+-----+-----+ 1226
TCCATCCTGGTACCGTCTGCTCTGGG

```

41/111

Figure 13. Restriction enzyme analysis of the *C. pneumoniae* Endopeptidase gene (SEQ ID NO: 5).

42/111

Figure 13 (Cont.)

```

                                MaeIII
                                CviRI |
                                AlwI  | |
                                BpmI  | |
                                Hpy188IX | | |
                                MboII | | |
                                DpnI  | | | |
                                TaqI   BstYI | | | | |
                                DpnI | Sau3AI | | | | |
                                Sau3AI | | BsaBI | | | | |
                                | | | | | | | | |
                                ATTGATCGAAGATATGGATCTGATTGCAGTAACGCAAACCTCCAGGGTTGATAGGTTCCTCT
301 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 360
                                TAACTAGCTTCTATACCTAGACTAACGTCATTGCGTTTGAGGTCCCAACTATCCAAGAGA

                                CviRI      BsrDI      MwoI      HinfI
                                |          |          |          |
                                ATCAGTAGGAGTGCAATTTTGGTAAAGGCATTGCCATAGGAGCAAAAAAATCCTTGATTGG
361 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 420
                                TAGTCATCCTCACGTAAAACCATTTCGTAACGGTATCCTCGTTTTTTTAGGAACCTAACC

                                Tsp509I
                                CviRI |
                                BbvI  | |
                                TaqI   BtrI | AluI      Fnu4HI  BstAPI | |
                                MaeII | CviJI      Fnu4HI  BglI  | | MwoI | |
                                PleI | | BbvI | MsI | TseI | MwoI | | HhaI | | | |
                                | | | | | | | | | | | | | | | |
                                AGTCAATCACGTCGAAGCTCATCTCTATGCTGCCTATATGGCAGCGCAAAACGTGCAATT
421 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 480
                                TCAGTTAGTGCAGCTTCGAGTAGAGATACGACGGATATACCGTCGCGTTTTTGCACGTTAA

                                BanII
                                BsiHKAI
                                Bsp1286I
                                SacI
                                AluI |
                                CviJI | Fnu4HI
                                BsaI  | | TseI | BbvI
                                BsmAI | | AciI | | FokI |
                                BslI   Hpy178III | | MwoI | | BpmI | |
                                EcoNI | | | | | | | | |
                                | | | | | | | | |
                                CCCTGCTTTAGGTCTTGTGGTCTCTGGAGCTCATACCGCAGCGTTTTTTATAGAAAATCC
481 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 540
                                GGGACGAAATCCAGAACACCAGAGACCTCGAGTATGGCGTCGCAAAAAATATCTTTTAGG

```

43/111

Figure 13 (Cont.)

```

                                Hpy178III
                                TaqI|
                                AvaI||
                                SmlI||
                                XhoI||
                                SfaNI |||      SfcI
                                | |||      |
541 TACATCCTATAAACTCATAGGAAAACTCGAGATGATGCTATAGGAGAACTTTTGATAA
-----+-----+-----+-----+-----+-----+-----+ 600
    ATGTAGGATATTTGAGTATCCTTTTTGAGCTCTACTACGATATCCTCTTTGAAAACTATT

                                Tsp509I
                                CviJI |
                                HaeIII |
                                Sau96I||
                                Cac8I||
                                PstI||
                                SbfI||
                                HgaI      CviRI ||| MseI
                                BfaI|      SfcI | ||| VspI|      BseMII
                                ||      | | |||      ||
601 AGTAGGACGCTTTCTAGGATTACCATACCTGCAGGCCCATTAATTGAAAACTCGCTTT
-----+-----+-----+-----+-----+-----+ 660
    TCATCCTGCGAAAGATCCTAATGGTATGGGACGTCCGGTAATTAACCTTTTGAGCGAAA

                                Hpy188IX      BsmFI
                                DdeI|      Bsp24I |      AluI
                                CviJI ||      CjePI |      CviJI      CjeI
                                MnlI | || Bst4CI CjeI| | BspGI |      Bsp24I|
                                | | ||      | || |      | |
661 AGAAGGCTCTGAGGACAGTTATCCTTTTAGTCCAGCTAAAGTCCCAAATATGACTTTTC
-----+-----+-----+-----+-----+-----+ 720
    TCTTCGAGACTCCTGTCAATAGGAAATCAGGTCGATTTTCAGGGTTTGATACTGAAAAG

                                AluI
                                CviJI
                                AcII      MspAII      BsrBI
                                MspAII MseI PvuII      BpmI | |
                                |      |      CviJI | |
                                |      |      | |
721 ATTCAGCGGTCTTAAACAGCTGTTCTCTACGCAATCAAAGGAAATAATAGTAGCCCCCG
-----+-----+-----+-----+-----+-----+ 780
    TAAGTCGCCAGAATTTTGTGACAAGAGATGCGTTAGTTTCCTTTATTATCATCGGGGGC

                                Hpy178III      Fnu4HI
                                FauI |      TseI|
                                Sth132I| | EcoRV      BbvI      EcoRV || BsgI
                                | |      |      |      |
781 CTCTCCTGCTCCAGAGATATCTTTAGAAAAACAAAGAGATATCGCTGCTTCATTTCAAAA
-----+-----+-----+-----+-----+-----+ 840
    GAGAGGACGAGGTCTCTATAGAAATCTTTTGTCTCTATAGCGACGAAGTAAAGTTTT

```

44/111

Figure 13 (Cont.)

```

      CviRI
      Cac8I |
      CviJI | |
      HaeIII | |
      Fnu4HI | | |
      TauI | | |
      AciI | | | |      CviRI      PsiI      Sau3AI
      || | | |      |      |      |
      AGCGGCCTGCACTACTATTGCACAAAACTTCCCACATTATATAAAAGAATTTTCGTGCCG
841 -----+-----+-----+-----+-----+-----+-----+ 900
      TCGCCGGACGTGATGATAACGTGTTTTGAAGGGTGATAATATTTTCTTAAAGCACGGC

      AciI
      DpnI |
      MseI      BstYI | |
      VspI      Sau3AI | |
      DpnI      MnlI      BsaXI      CviJI      |      AlwI      | | |
      |      |      |      |      |      |      |      |
      ATCTATACTTATTGGAGGTGGCGTAGCCATTAATGAATACTTTAGATCCGCAATACAAAC
901 -----+-----+-----+-----+-----+-----+-----+ 960
      TAGATATGAATAACCTCCACCGCATCGGTAATTACTTATGAAATCTAGGCGTTATGTTTG

      BstZ17I      Hpy188IX      BseMII
      MjaIV      DdeI |      BspMI |
      AccI |      BbvI | |      Fnu4HI ||
      ||      | | |      TseI | ||
      TCGTGTAATCTACCTGTATACTTCCCCCCTGCTAAACTATGCTCAGATAATGCTGCTAT
961 -----+-----+-----+-----+-----+-----+-----+ 1020
      ACGCACATTAGATGGACATATGAAGGGGGGACGATTGATACGAGTCTATTACGACGATA

      ApoI
      Tsp509I
      CviRI      Hpy178III |
      HaeIV      XmnI      MspI |
      Hin4I      ApoI |      BsaWI |
      MwoI | BfaI      Tsp509I |      BfaI      Kpn2I |
      | |      | |      | |      | |
      GATTGCAGGTCTAGGGGGAGAAAATTTTCAAAAAAACTCTAGTATTCGGAAATTCGTAT
1021 -----+-----+-----+-----+-----+-----+-----+ 1080
      CTAACGTCCAGATCCCCCTCTTTTAAAAGTTTTTTTGAGATCATAAGGCCTTTAAGCATA

      HphI
      HinfI |
      HhaI      TfiI |
      FspI | EcoRV      TspRI |
      ||      |      ||
      ATGCGCAAGATATCAGTGGGAATCTGTATCACCATTCTCCTTAGCCTCTCCGTAGTCCCTC
1081 -----+-----+-----+-----+-----+-----+-----+ 1140
      TACGCGTTCTATAGTCACCCTTAGACATAGTGGTAAGAGGAATCGGAGAGGCATCAGGAG

```



45/111

Figure 13 (Cont.)

```

                                PleI
                                MaeIII |
                                CviRI   Tsp45I |
                                MnlI|   BspGI | |
                                Fnu4HI||   BsrI | |
                                CviJI|||   BseRI | | |   MnlI           MseI
                                TseI|||HinfI | | | |Sth132I   AvaI|           VspI
                                ||| | | | | | | | | | | | | | |
1141 CAAGGCTGCAAGGAGTCCAGTCACTCCTCTACATCTCGGGGAGAACTCGCTATTAATATA
-----+-----+-----+-----+-----+-----+-----+ 1200
GTTCCGACGTTCTCAGGTCAGTGAGGAGATGTAGAGCCCCTCTTGAGCGATAATTATAT

```

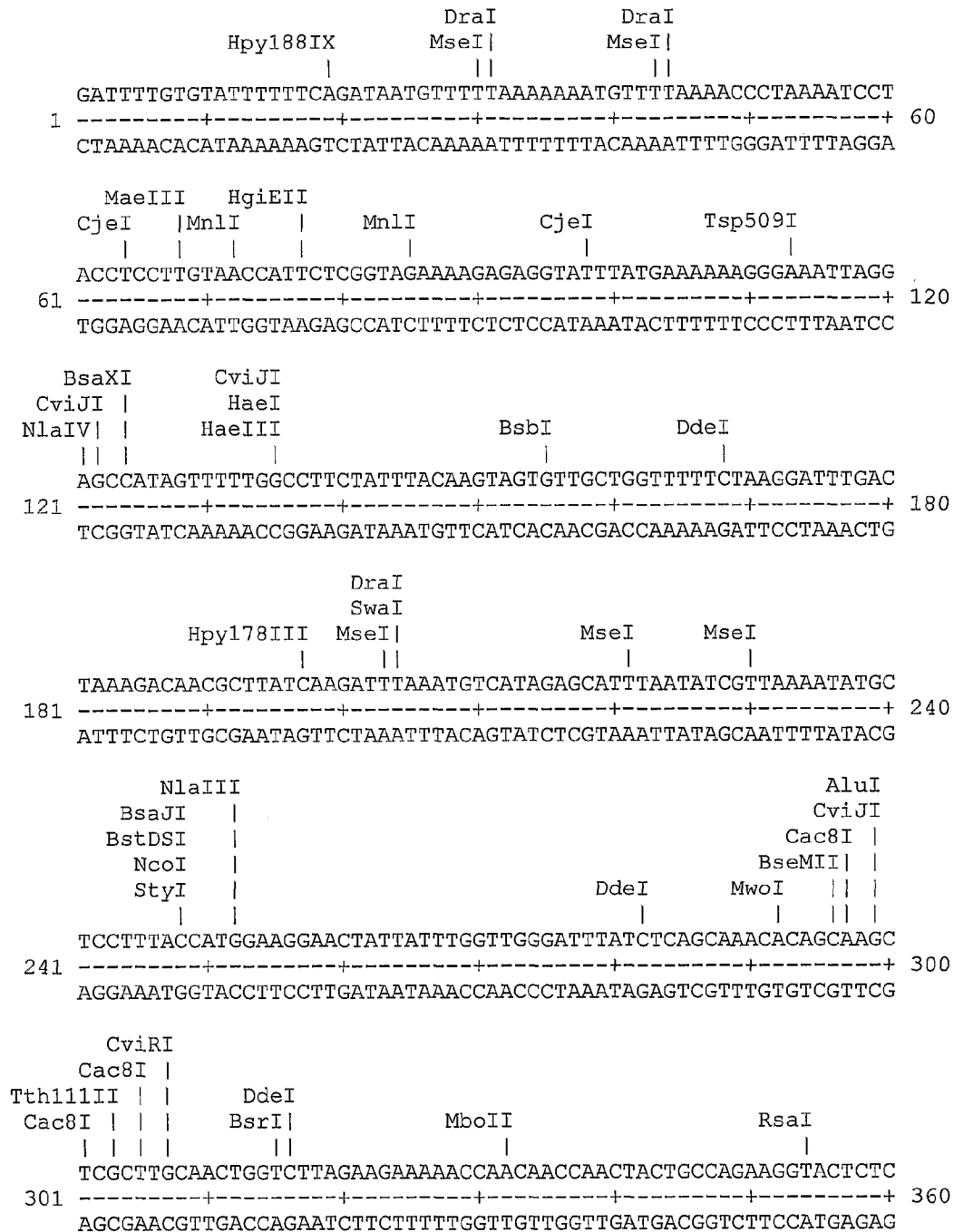
```

                                DpnI
                                BstYI |
                                Sau3AI |
                                Sth132I | |
                                AlwI | | |
                                CjeI | | |
                                BscGI | | | |
                                | | | | |
1201 AGAGATGAACCCCGTTCTTTAGATCCAAGACAAGT
-----+-----+-----+-----+-----+ 1235
TCTCTACTTGGGGCAAGAAATCTAGGTTCTGTTC

```

46/111

Figure 14. Restriction enzyme analysis of the *C. pneumoniae* Protease gene (SEQ ID NO: 7)



47/111

Figure 14 (Cont.)

```

          DpnI
          BcgI |
          Sau3AI |
          BsaAI | |
          MaeII| | |MseI          CviRI          BcgI
          || | | |          NlaIII          MaeII | | RsaI
          || | | |          |          | | |
361 TAACTACGTGAGATCATTAAACGATTATCATGCAGGGATTACGTTTATCGTACTGAAAG
-----+-----+-----+-----+-----+-----+-----+
ATTGATGCACTCTAGTAATTTGCTAATAGTACGTCCCTAATGCAAAATAGCATGACTTTC

          RsaI
          MaeII |
          HincII | |
          MjaIV | |
          BsaAI          AccI | |
          SnaBI          TaqI | |
          MaeII|          MboII          NlaIII          SalI|| | |
          || |          |          |          || | | |
421 TCGGTATATCCCTTACGTATTGAAGTTAAGTGAAGATGGTCATGTCTTTGTAGTCGACGT
-----+-----+-----+-----+-----+-----+
ACGCATATAGGGAATGCATAACTTCAATTCACCTTCTACCAGTACAGAAACATCAGCTGCA

          BsaJI
          StyI
          CviJI|
          BfaI ||          DdeI          FokI          BccI
          | ||          |          |          |
481 ACAGACTAGCCAAGGGGATATTTACTTAGGGGATGAAATCCTTGAAGTAGATGGAATGGG
-----+-----+-----+-----+-----+-----+
TGTCTGATCGGTTCCCTATAAATGAATCCCCTACTTTAGGAACTTCATCTACCTTACCC

          Hpy178III
          HinfI |
          MnlI |          TaqI CviJI
          TfiI | CviJI | XmnI          MnlI          BbvI          Fnu4HI
          | | | | |          |          |          |          SfcI
          | | | | |          |          |          |          TseI|
          | | | | |          |          |          |          ||
541 GATTCGTGAGGCTATCGAAAGCCTTCGCTTTGGACGAGGGAGTGCCACAGACTATTCTGC
-----+-----+-----+-----+-----+-----+
CTAAGCACTCCGATAGCTTTTCGGAAGCGAAACCTGCTCCCTCACGGTGTCTGATAAGACG

          Tsp509I
          Eco57I          Hpy178III |
          SfaNI |          NlaIV | |
          AciI| |          AciI | |
          Fnu4HI| |          AfoI | |
          TauI| |          PpiI | |
          PstI          EciI          ThaI          AciI || | BsaXI| | |
          CviRI |          |          |          || | |
          | |          |          |          || | |
601 TGCAGTTCGTTTCCTTGACATCGCGTTCCGCCGCTTTTGGAGATGCGGTTTCCTTCAGGAAT
-----+-----+-----+-----+-----+-----+
ACGTCAAGCAAGGAACTGTAGCGCAAGGCGGCGAAAACCTCTACGCCAAGGAAGTCCTTA

```

48/111

Figure 14 (Cont.)

```

                                     BpmI
                                     AvaII |
                                     RsrII |
                                     Sau96I |
                                     DpnI
                                     Sau3AI |
                                     TspRI | |
                                     AlwI | | |
                                     BmrI | | | |
                                     BsrI | | | | |
                                     NlaIII   SimI | | | | | | |   TaqI   | | | |   CjePI
                                     | | | | | | |   | | | |   |
TGCCATGTTGAAACTTCGCCGACCCAGTGGTTTGATCCGTTTCGACACCGGTCCGTTGGCG
661 -----+-----+-----+-----+-----+-----+-----+ 720
ACGGTACAACCTTTGAAGCGGCTGGGTCACCAAAGTAGGCAAGCTGTGGCCAGGCAACCGC

                                     Hpy178III
                                     HinfI |
Hpy178III   Hpy188IX   CjePI   TfiI |
| | | | |
TTATACTCCAGAGCATATCGGAGATTTTCTTTAGTTGCTCCTTTGATTCCTGAACATAA
721 -----+-----+-----+-----+-----+-----+-----+ 780
AATATGAGGTCTCGTATAGCCTCTAAAAAGAAATCAACGAGGAACTAAGGACTTGTATT

                                     BbsI
                                     MboII
                                     ApoI |
                                     Tsp509I |
                                     BslI | |
                                     NciI | |
                                     ScrFI | |
                                     BsaJI | |
Tsp509I   MnlI   Sth132I   MspI | | | | Bst4CI   BfaI
| | | | | | | | | | | | | | | | |
ACCTCAATTACCTACACAAAGTTGTGTGCTATTCCGTTCCGGGGTAAATTCACAGTCTTC
781 -----+-----+-----+-----+-----+-----+-----+ 840
TGGAGTTAATGGATGTGTTTCAACACACGATAAGGCAAGGCCCAATTTAAGTGTCAGAAG

                                     NlaIV
                                     BanI |
                                     AluI   NlaIII |
CviJI   | | | | |
TAGTAGCTCTTTATTTCAGTTCCTACATGGTGCCTTATTTCTGGGAAGAATTGCGGGTTCA
841 -----+-----+-----+-----+-----+-----+-----+ 900
ATCATCGAGAAATAAGTCAAGGATGTACCACGGAATAAAGACCCTTCTTAACGCCCAAGT

                                     Bst4CI
Fnu4HI   BbvI | CjePI   CviJI
TseI | HphI | | BceFI | NlaIV | MaeII
| | | | | | | | | | |
AAATAAGCAGCGTTTTGACAGTAATCACCATATAGGGAGCCGTAATGGATTTTTACCTAC
901 -----+-----+-----+-----+-----+-----+-----+ 960
TTTATTTCGTCGCAAACTGTCATTAGTGGTATATCCCTCGGCATTACCTAAAAATGGATG

```

49/111

Figure 14 (Cont.)

```

                                ApaI
                                BanII
                                BseSI
                                Bsp1286I
                                BmgI |
                                CviJI |
                                HaeIII |
                                NlaIV |
                                EcoO109I| |
                                NlaIV| |
AvaII
Sau96I
BslI |
CjePI| |
|| |
                                EcoO109I|| |
                                Sau96I|| |
                                || |
                                DraI
                                MseI|
                                ||
961  GTTTGGTCCTATTCTTTGGGAACAAGACAAGGGGCCCTATCGTTCCTATATCTTTAAAGC
-----+-----+-----+-----+-----+-----+-----+-----+ 1020
    CAAACCAGGATAAGAAACCCTTGTTCTGTTCCCCGGGATAGCAAGGATATAGAAATTTTCG

                                XmnI
                                Tth111III|
                                ApoI  ||
                                Tsp509I ||
HinfI |
TfiI  |
|     |
                                BccI
                                BseMII
                                MboII |
                                MseI| |
                                || |
1021 AAAAGATTCTCAGGGCAATCCCCATCGCATAGGATTTTAAAGAATTTCTTCTTATGTTTG
-----+-----+-----+-----+-----+-----+-----+ 1080
    TTTTCTAAGAGTCCCGTTAGGGGTAGCGTATCCTAAAAATTCTTAAAGAAGAATACAAAC

                                BanII
                                BsiHKAI
                                Bsp1286I
                                SacI
                                DpnI
                                MnlI
                                CjePI|
                                EarI|
                                ||
                                AlwI
                                BsaJI
                                StyI
                                ||
                                AluI |
                                CviJI |
                                ||
                                Sau3AI
                                CjePI|
                                ||
1081 GACTGATTTAGAAGGACTTGAAGAGGATCATAAGGATAGTCCTTGGGAGCTCTTTGGAGA
-----+-----+-----+-----+-----+-----+-----+ 1140
    CTGACTAAATCTTCCTGAACTTCTCCTAGTATTCCTATCAGGAACCCTCGAGAAACCTCT

                                DpnI
                                Sau3AI |
                                ClaI| |
                                TaqI| |
                                HaeIV|| |
                                Hin4I|| |
                                DpnI ||| |
                                Hin4I| ||| |
                                || ||| |
                                SfaNI
                                BsmAI |
                                || |
                                Hpy188IX
                                SimI
                                DpnI |
                                BclI |
                                Sau3AI |
                                HaeIV |
                                Hin4I |
                                || |
                                ScrFI
                                BstXI|
                                EcoRII||
                                MnlI |||
                                HaeIV |
                                Hin4I |
                                || |
1141 GATCATCGATCATTTGGAAAAAGAGACTGATGCTTTGATTATTGATCAGACCCATAATCC
-----+-----+-----+-----+-----+-----+-----+ 1200
    CTAGTAGCTAGTAAACCTTTTCTCTGACTACGAAACTAATAACTAGTCTGGGTATTAGG

```

50/111

Figure 14 (Cont.)

```

                                DpnI
                                Sau3AI |
                                HincII | |
                                HpaI  | |
                                MjaIV  | |
                                BtsI    | |
                                BsaXI|TspRI  BpmI  | | FokI MseI | |
                                ||  |  |  |  |  |  |
TGGAGGCAGTGTTTCTATCTCTATTTCGTTACTATCTATGTTAACAGATCATCCTTTAGA
1201 -----+-----+-----+-----+-----+-----+ 1260
ACCTCCGTCACAAAAGATAGAGATAAGCAATGATAGATACAATTGTCTAGTAGGAAATCT

                                AceIII
                                CviJI  |
                                FokI   | |
                                Hpy178III AluI | | |
                                DdeI    | | CviJI | | | BsrI
                                Hin4I   | | BseMII| | |CviRI TspRI
                                |  |  |  |  |  |  |
TACTCCTAAACATAGAATGATTTTCACTCAGGATGAAGTCAGCTCGGCTTTGCACTGGCA
1261 -----+-----+-----+-----+-----+-----+ 1320
ATGAGGATTTGTATCTTACTAAAAGTGAGTCCTACTTCAGTCGAGCCGAAACGTGACCGT

DpnI
BglII | BbsI
BstYI | MboII
Sau3AI | BfaI | MboII | Cac8I BslI BfaI CjePI
|  |  |  |  |  |  |  |  |
AGATCTACTAGAAGATGTCTTCACAGATGAGCAGGCAGTTGCCGTGCTAGGGGAAACTAT
1321 -----+-----+-----+-----+-----+-----+ 1380
TCTAGATGATCTTCTACAGAAGTGCTACTCGTCCGTCAACGGCACGATCCCCTTTGATA

                                CviJI
                                CjePI |
                                MboII| |
                                SfcI  || |
                                NlaIII| || |
                                NspI  || |
                                SphI  || |
                                MslI  Cac8I || || |
                                NlaIII| NsiI || || |
                                CviRI  ||CviRI || || |
                                |  ||  || || || |
GGAAGGATATTGCATGCATATGCATGCTGTAGCCTCTCTTCAAACTTCTCTCAGAGTGT
1381 -----+-----+-----+-----+-----+-----+ 1440
CCTTCCTATAACGTACCTATACGTACGACATCGGAGAGAAGTTTGAAGAGAGTCTCACA

```

51/111

Figure 14 (Cont.)

```

          ScrFI
          BsaJI|
          EcoRII||
BseMII  |||
          |  |||
CCTTTCTTCTGGGTTTCAGGTGATATTAACCTTTCAAACCTATGCCTTTGCTAGGATT
1441 -----+-----+-----+-----+-----+-----+ 1500
          GAAAGAAGACCCAAAGTCCACTATAATTGGAAAGTTTTGGATACGGAAACGATCCTAA

          FokI
CviRI|  TaqI      MnlI      MnlI
  ||    |          |          |
TGCACAGGTTTCGACCTCATCCTAAACATCAATATACTAAACCTTTGTTTATGTTGATAGA
1501 -----+-----+-----+-----+-----+-----+ 1560
          ACGTGTCCAAGCTGGAGTAGGATTTGTAGTTATATGATTTGGAAACAAATACAACATATCT

                                          HhaI
                                          ThaI |
                                          AciI | |
                                          Fnu4HI | |
                                          TauI | |
                                Tsp509I
                                CviRI|
                                CjePI||
                                Cac8I|||
                                HaeII||||
                                HhaI|||||
          Hin4I      FokI      HhaI|||||      GdiII | | | |
          |          |          | | | | |          | | | |
CGAGGATGACTTCTCTTGTGGAGATTTAGCGCCTGCAATTTGAAGGATAATGGCCGCGC
1561 -----+-----+-----+-----+-----+-----+ 1620
          GCTCCTACTGAAGAGAACACCTCTAAATCGCGGACGTTAAAACTTCCTATTACCGGCGCG

          AluI
          AlwNI
          CviJI
          CjeI |
          CviJI      MnlI |
          CjePI  AceIII|  BslI | |  BsaXI      BpmI
          |          ||          | |          |      MaeIII |
          |          |          | |          |      Tsp45I |
TACTCTCATTGGAAAGCCAACAGCAGGAGCTGGAGGTTTTGTATTCCAAGTCACTTTCCC
1621 -----+-----+-----+-----+-----+-----+ 1680
          ATGAGAGTAACCTTTCGGTTGTCGTCCTCGACCTCCAAAACATAAGGTTTCAGTGAAAGGG

          MseI
          Tsp509I |
          Hpy178III | |
          Bst4CI  | | |
          |  |  |  |
          TAACCGTTCTGGAATTAAAGGTCTTTCTTTAACAGGATCTTTAGCTGTTAGGAAAGATGG
1681 -----+-----+-----+-----+-----+-----+ 1740
          ATTGGCAAGACCTTAATTTCCAGAAAGAAATTGTCCTAGAAATCGACAATCCTTTCTACC

          DpnI
          BstYI |
          Sau3AI |
          MseI  | |
          |  |  |
          AluI
          CviJI
          AlwI |
          BccI

```

52/111

Figure 14 (Cont.)

```

                                BseRI   NlaIV   MnlI   ScrFI
                                HphI DdeI |   CviJI |   BpmI |   BsaJI |
                                |   |   |   |   |   |   |   |
TGAGTTTATTGAAACTTAGGAGTGGCTCCTCATATTGATTTAGGATTTACCTCCAGGGA
1741 -----+-----+-----+-----+-----+-----+ 1800
ACTCAAATAACTTTTGAATCCTCACCGAGGAGTATAACTAAATCCTAAATGGAGGTCCCT

                                SfcI
                                TspRI |   BseMII
MnlI | EcoRII | MjaIV   MnlI |   BtsI |   |   MseI |
|   |   |   |   |   |   |   |   |   |   |
TTTGCAAACCTCCAGGTTTACTGATTACGTTGAGGCAGTGAAACTATAGTTTAACTTC
1801 -----+-----+-----+-----+-----+-----+ 1860
AAACGTTTGAAGGTCCAAATGACTAATGCAACTCCGTCACCTTTTGATATCAAATGAAG

                                AciI
                                BsmAI
Hpy188IX   DdeI   EarI   BsmBI   BsaHI   XmnI
DdeI |   EarI |   SapI   MboII   MboII |   MwoI |   HgaI |
|   |   |   |   |   |   |   |   |   |   |
TTTGTCTGAGAACGCTAAGAAGAGTGAAGAGCAGACTTCTCCGCAAGAGACGCCTGAAGT
1861 -----+-----+-----+-----+-----+-----+ 1920
AAACAGACTCTTGCGATTCTTCTCACTTCTCGTCTGAAGAGGCGTTCTCTGCGGACTTCA

                                Eco57I
                                MaeII
HinfI   PleI |   RleAI   BscGI |   BsmFI
TaqI |   BsmAI |   Sth132I | MjaIV |   |   Tsp509I
|   |   |   |   |   |   |   |   |   |   |
TATTCGAGTCTCTTATCCCACAACGACTTCTGCTTCGTAAACGGGACGTAATAGAATAAT
1921 -----+-----+-----+-----+-----+-----+ 1980
ATAAGCTCAGAGAATAGGGTGTGCTGAAGACGAAGCATTTGCCCTGCATTATCTTATTA

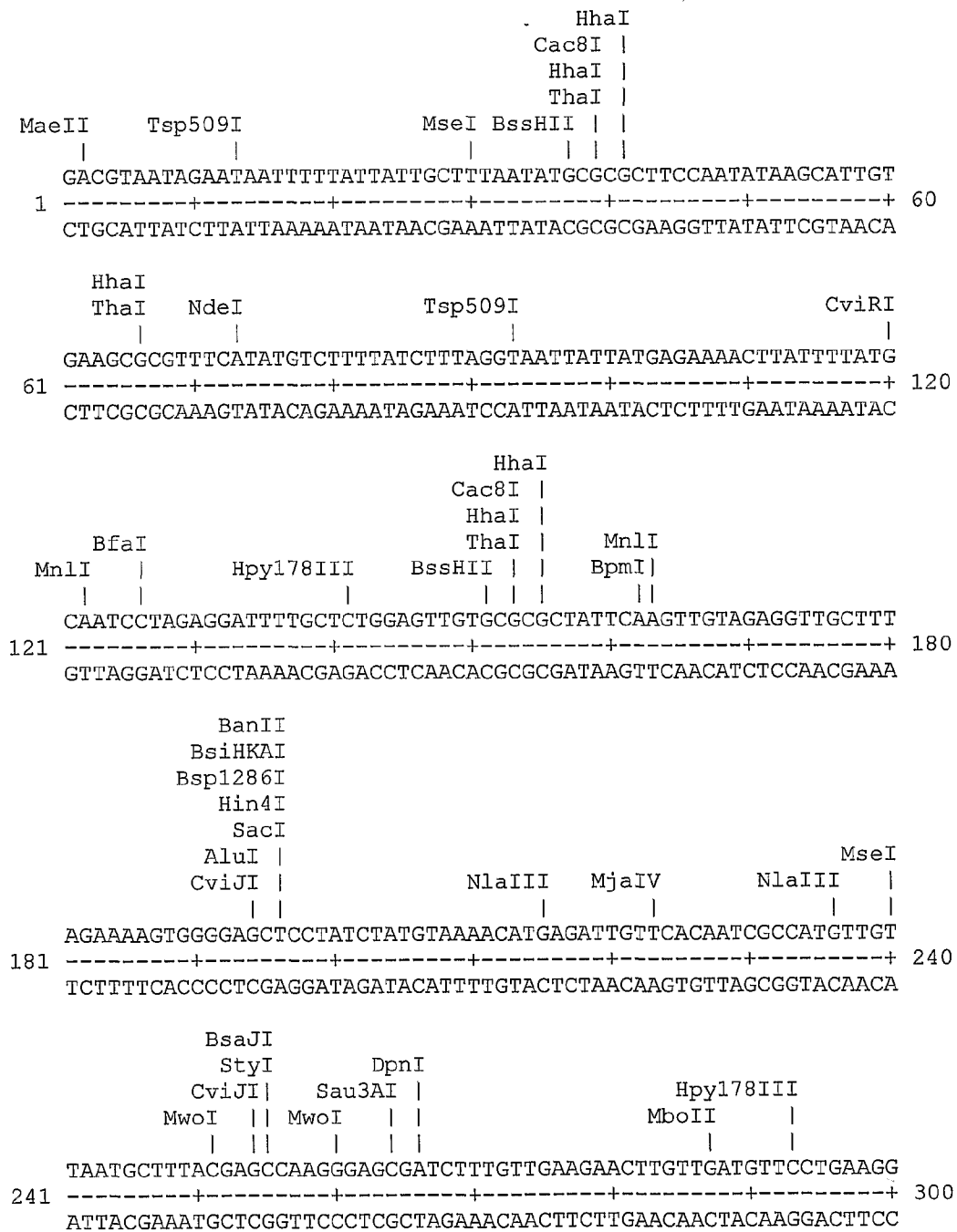
                                HhaI
                                Cac8I |
                                HhaI |
                                ThaI |
                                MseI BssHII |   |   HhaI
                                |   |   |   |   |   |   |   |
TTTTATTATTGCTTTAATATGCGCGCTTCCAATATAAGCATTTGTGAAGCGCGTTTCATAT
1981 -----+-----+-----+-----+-----+-----+ 2040
AAAATAATAACGAAATTATACGCGCGAAGGTTATATTCGTAACACTTCGCGCAAAGTATA

GTCTTTTATCTTTAGGTAAT
2041 -----+-----+ 2060
CAGAAAATAGAAATCCATTA

```



53/111

**Figure 15: Restriction enzyme analysis of the *C. pneumoniae* Metalloprotease gene (SEQ ID NO: 9).**

54/111

Figure 15 (Cont.)

```

                                AceIII
                                AceIII |
                                ApoI  | |
                                EcoRI  | |
                                Tsp509I | |
                                NlaIII | | |
                                Eco57I  | | | |
                                Eco57I  | | | |
                                PleI | AluI | | |
                                HinfI HphI || CviJI | | | |
                                | | | | | | | | | |
                                TGAGAGAGTCATTTATTCAGCTCATGGAATTCCTCCTTCAGTTAGAGCTGAAGCAAAAGC
301 -----+-----+-----+-----+-----+-----+ 360
                                ACTCTCTCAGTAAATAAGTCGAGTACCTTAAGGAGGAAGTCAATCTCGACTTCGTTTTTCG

                                SfaNI
                                Eco57I |
                                AluI  ||
                                CviJI  ||
                                Sth132I ||
                                HindIII | ||
                                BscGI   | | | |
                                | | | |
                                CCGTAAGCTTATTGATATTGATGCTACCTGTGGTTTGGTTACTAAGGTGCATTCTGCTGC
361 -----+-----+-----+-----+-----+-----+ 420
                                GGCATTTCGAATAACTATACTACGATGGACACCAAACCAATGATTCCACGTAAGACGACG

                                CviJI
                                HaeIII
                                EaeI  |
                                GdiII |
                                HaeIV  |
                                DpnI  | |
                                BciVI  | | | |
                                | | | |
                                GAAGTTATACGCAAGTAAAGGATACAAAATCATACTGATCGGCCATAAGAAGCACGTTGA
421 -----+-----+-----+-----+-----+-----+ 480
                                CTTCAATATGCGTTCATTTCTATGTTTTAGTATGACTAGCCGGTATTCTTCGTGCAACT

                                Hpy178III
                                Bst4CI |
                                HphI  | Hpy178III BcgI | TaqI |
                                | | | | |
                                GGTGATTGGTATTGTTGGAGAAGTTCCTGAACACATTACTGTTGTGCGAGAAGGTTGCTGA
481 -----+-----+-----+-----+-----+-----+ 540
                                CCACTAACCATAACAACCTCTTCAAGGACTTGTGTAATGACAACAGCTCTTCCAACGACT

```

55/111

Figure 15 (Cont.)

```

      BcgI
      CviJI|
      HaeI|
      HaeIII|
AatII  ||
TaqI  StuI|      Hpy188IX      MaeII
      ||      |
CGTCGAGGCCTTACCTTTTAGTTCTGATACACCTTTATTTTATATTACTCAAACGACGTT
541 -----+-----+-----+-----+-----+-----+ 600
GCAGCTCCGGAATGGAAAATCAAGACTATGTGGAAATAAAATATAATGAGTTTGCCTGCAA

      Hin4I
      DpnI|
      BglII ||
      BstYI ||
      Sau3AI ||
      FokI| ||
      Hpy178III || || CviJI      EcoRV
      | || || |
GAGTTTGGATGATGTTTCAGGAGATCTCATCGGCTTTGCTAAAGCGATATCCCTCTATCAT
601 -----+-----+-----+-----+-----+-----+ 660
CTCAAACCTACTACAAGTCCTCTAGAGTAGCCGAAACGATTTGCTATAGGGAGATAGTA

      CviRI
      BfaI      Bsp24I |
      MboII |      CjePI |
      MnlI | |      TaqI CjeI| |      Bst4CI      BsrDI Bsp24I|
      | | | |      || |
TACTCTGCCTAGTTCTTCGATTTGTTATGCAACCACGAACCGTCAAAAAGCATTTGCGTTC
661 -----+-----+-----+-----+-----+-----+ 720
ATGAGACGGATCAAGAAGCTAAACAATACGTTGGTGCTTGGCAGTTTTTCGTAACGCAAG

      AceIII
      BbsI |
      MboII |
      ApoI | |
      EcoRI | |
      Tsp509I | |
      TaqI | | |
      CjePI| | |
      AluI|| | |
      CviJI|| | |
      Tsp509I
      MmeI |      HincII ||| | | |
      ThaI| |MaeII      MjaIV ||| | | |
      || | |
TGTTTTATCTCGCGTGAATTACGTCTATGTGGTTGGAGATGTCAACAGCTCGAATTCCAA
721 -----+-----+-----+-----+-----+-----+ 780
ACAAAATAGAGCGCACTTAATGCAGATACCAACCTCTACAGTTGTGAGCTTAAGGTT

```

56/111

Figure 15 (Cont.)

```

                                                    BsaJI
                                                    AvaI|
                                                    Hpy178III|
                                                    MnlI   ||
                                                    HaeIV  |  ||
                                                    Hin4I  |  ||
                                                    DpnI   |  ||
                                                    BclI   |  ||
                                                    Sau3AI |  ||
                                                    FauI   |  ||
                                                    Sth132I|  ||
NruI                                     MspA1I  ||  ||  ||  ||
ThaI                                     AciI   |  ||  ||  ||  ||
Hpy178III|   CviJI   |   |   |   |   |   |   |
      ||       |   |   |   |   |   |   |   |
TCGTCTTCGCGAAGTGGCTTTGAGAAGGGGAGTTCCCGCTGATTGATCAACAATCCCCGA
781 -----+-----+-----+-----+-----+-----+-----+ 840
AGCAGAAGCGCTTCACCGAAACTCTTCCCTCAAGGGCGACTAACTAGTTGTTAGGGCT

                                                    CviJI
                                                    NlaIV|
                                                    PstI   ||
                                                    BpmI   ||
                                                    CviRI  ||  ||
                                                    BsrDI  |||  ||
                                                    SfcI   |||  ||
                                                    BstAPI |||  ||
Sth132I                                     Hpy178III   MwoI |||  ||
      |                                     |               |||  |||  ||
GGATATTGATACGAACATCGTAAATCATTCTGGAGATATAGCAATGACTGCAGGAGCCTC
841 -----+-----+-----+-----+-----+-----+-----+ 900
CCTATAACTATGCTTGTAGCATTTAGTAAGACCTCTATATCGTTACTGACGTCTCTCGGAG

                                                    BsmI
                                                    CviRI
                                                    Cac8I  |
                                                    AluI   |  |
                                                    CviJI  |  |
                                                    HindIII|  |  |
                                                    BbsI   |  |  |
                                                    MaeII  |  |  |
                                                    Sth132I|  |  |
MnlI   |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Hpy178III |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
AACTCCCGAAGACGTAGTTCAAGCTTGCATTGCGAAAGCTATCATCACTTATCCCTGGTTT
901 -----+-----+-----+-----+-----+-----+-----+ 960
TTGAGGGCTTCTGCATCAAGTTCGAACGTAAGCTTTTCGATAGTAGTGAATAGGGACCAA

```

57/111

Figure 15 (Cont.)

```

                                FokI
                                Tsp509I
                                CjePI |
                                | |
                                | |
SfcI
MnlI |
| |
ACAAGTGGAAAATGATATATTTGCTGTAGAGGATGTCGTATTTCAATTACCAAAGAAGT
961 -----+-----+-----+-----+-----+-----+ 1020
TGTTCACCTTTTACTATATAAACGACATCTCCTACAGCATAAAGTTAATGGTTTTCTTGA

                                Hpy178III
                                TaqI|
                                AvaI||
                                Hpy178III||
                                SmlI||
                                XhoI||
                                |||
DdeI CjePI CviJI
| | |
CCGTTGTTCTTAGGTCTTTAGGCTTACTTGCCAAGTTTTTCTCGAGATTGCTTTATAGAG
1021 -----+-----+-----+-----+-----+-----+ 1080
GGCAACAAGAATCCAGAAATCCGAATGAACGGTTCAAAAAGAGCTCTAACGAAATATCTC

                                Hpy188IX
                                PleI MnlI |
                                | | |
TCTTCTTCTCGTTCAGAGAGGGTATTTACCTTTTITAGTTCTCTGTATTTGAAA
1081 -----+-----+-----+-----+-----+-----+ 1133
AGAAGAAGAGCAAGTCTCTCCATAAATGGAAAAATCAAGAGACATAAACTTT

```

58/111

**Figure 16: Restriction enzyme analysis of the *C. pneumoniae* CLP protease ATPase gene (SEQ ID NO: 11).**

BsaJI

```

          CviJI |
          NlaIV ||
MnlI   |||   BccI
NlaIII |||   MwoI | |
          | | |   | |
CATGGGAGCCGAGGAAGCCATCTCCTACGGACTTATTGATAAGGTGGTAACTTCTGCGAA
1  -----+-----+-----+-----+-----+-----+ 60
GTACCCCTCGGCTCCTTCGGTAGAGGATGCCTGAATAACTATTCCACCATGAAGACGCTT

          BciVI           DdeI           NdeI
          |               |               |
AGAAACTAATAAGGATACAAGTAGCACTTAGAGAGAACATATGAATAAAAAAATCTAAC
61 -----+-----+-----+-----+-----+-----+ 120
TCTTTGATTATTCCTATGTTTCATCGTGAATCTCTCTTGATACTTATTTTTTTAGATTG

          Hpy188IX           CviJI
          BsiEI |           HaeIII
          TaqII AciI | |           Sau96I |
          | | | |           | |
TATTGTTCATTTTGCGGTCGGTCTGAAAAAGATGTAGAGAACTGATTGCTGGGCCTTC
121 -----+-----+-----+-----+-----+-----+ 180
ATAACAAGTAAAACGCCAGCCAGACTTTTCTACATCTCTTTGACTAACGACCCGGAAG

          ApoI
          Tsp509I
          Hpy178III |
          SfaNI | |
BstZ17I MjaIV MaeIII Tsp509I | | |
AccI | Tsp45I CviRI | | | BseRI
| | | | | |
GGTATACATTTGTGACTACTGCATCAAATTATGCTCTGGAATTTTAGATAAGAAACCTC
181 -----+-----+-----+-----+-----+-----+ 240
CCATATGTAAACACTGATGACGTAGTTTAATACGAGACCTTAAAATCTATTCTTTGGGAG

```

59/111

Figure 16 (Cont.)

```

Hpy188IX
AceIII|
BseMII|
AlwNI||
MnII |||
BsrI | |||
AluI | | |||
CviJI | | |||
BbvCI | | | |||
Bpu10I | | | |||
DdeI | | | |||
MnII | | | | |||
MnII | | | | |||
BpmI | | | | | |||
CviJI | | | | | |||
CTCTACAATATCCTCAGCTCCAGTTTCTGAAACACCTTCACAGCCTTCTGATCTCAGGGT
241 -----+-----+-----+-----+-----+-----+-----+ 300
GAGATGTTATAGGAGTCGAGGTCAAAGACTTTGTGGAAGTGTCCGAAGACTAGAGTCCCA

Bsu36I
DdeI
BseMII | MslI Hpy178III AluI
CviJI
GCTTACCCCTAAGGAAATCAAAAAGCATATTGATGAATATGTCATTGGTCAGGAAAAGAC
301 -----+-----+-----+-----+-----+-----+-----+ 360
CGAATGGGGATTCCCTTTAGTTTTTTCGTATAACTACTTATACAGTAACCAGTCCTTTCTCG

BsiHKAI
Bsp1286I
BsaAI
MaeII|
BstZ17I || |
MjaIV || |
AccI| || |
PsiI MaeII || || |
TAAAAAGACAATCGCTGTTGCTGTTTATAATCACTATAAACGTATACGTGCTCTACTACA
361 -----+-----+-----+-----+-----+-----+-----+ 420
ATTTTTCTGTTAGCGACAACGACAAATATTAGTGATATTGTCATATGCACGAGATGATGT

```

Figure 16 (Cont.)

Hpy178III |  
 AlwNI |  
 DpnI ||  
 BstYI |||  
 Sau3AI |||  
 SfcI | | |  
 CviJI | | |  
 HaeIII | | |  
 EcoO109I | | |  
 Sau96I | | |  
 BscGI BfaI | | |  
 Tth111III AvrII | | |  
 AluI | BsaJI | | |  
 CviJI | CjeI | | |  
 Sth132I | MaeII StyI | | |  
 TAACAAACAGGTAAGCTACGGGAAATCTAACGTGCTTCTCCTAGGCCCTACAGGATCTGG  
 421 -----+-----+-----+-----+-----+-----+-----+ 480  
 ATTGTTTGTCCATTTCGATGCCCTTTAGATTGCACGAAGAGGATCCGGGATGTCTTAGACC  
 Tsp509I  
 MseI | CjeI ApoI  
 AlwI VspI | CviRI Tsp509I HphI CviJI  
 AAAAACATTAAATTGCAAAACATTGGCAAAATTTTAGATGTTCCCTTCACCATAGCCGA  
 481 -----+-----+-----+-----+-----+-----+-----+ 540  
 TTTTGTAAATTACGTTTTTGTAAACCGTTTTTAAATCTACAAGGGAAGTGGTATCGGCT  
 BspMI  
 HgaI | MboII BbvI  
 SimI | | HphI | MaeII  
 CGCAACGACCCTAACGGAAGCAGGTTATGTGCGGTGAAGATGTAGAGAACATTGTCTTACG  
 541 -----+-----+-----+-----+-----+-----+-----+ 600  
 GCGTTGCTGGGATTGCCTTCGTCCAATACAGCCACTTCTACATCTCTTGTAACAGAATGC  
 Fnu4HI Sth132I  
 AluI | CviRI | ClaI  
 CviJI | MnlI | TaqI  
 TseI | BscGI | | Hin4I BsgI |  
 TTTATTACAAGCTGCTGATTACGATGTGCGCCGTGCAGAACGAGGCATTATCTATATCGA  
 601 -----+-----+-----+-----+-----+-----+-----+ 660  
 AAATAATGTTTCGACGACTAATGCTACAGCGGGCACGTCTTGCTCCGTAATAGATATAGCT



Figure 16 (Cont.)

```

Tsp509I
ClaI |
TaqI |
| |
TGAAATCGATAAAATTGGAAGGACAAACAGCAAACGTCCTCCATTACTAGAGATGTTTCTGG
661 -----+-----+-----+-----+-----+-----+-----+ 720
ACTTTAGCTATTTTAACCTTCCTGTTGTGCGTTTGCAAGGTAATGATCTCTACAAAGACC

Tth111III DrdII AclI EcoNI
MseI | NlaIV| MaeII MnlI|
| | | |
CGAAGGGGTTCAACAAGCATTGTTAAAAATCGTTGAAGGAACACAGCAAACGTTTCCTCC
721 -----+-----+-----+-----+-----+-----+ 780
GCTTCCCCAAGTTGTTTCGTAACAATTTTTCAGCAACTTCCTTGCTGTCGTTTGCAAGGAG

MaeII
MnlI |
BslI| |
EcoNI || |
FokI || |
BslI| || | SfaNI Hpy188IX| PleI
|| || | | || |
TAAAGGAGGACGTAAGCATCCTAACCAAGAGTATATCCGAGTCAATACGGAAAAATATCTT
781 -----+-----+-----+-----+-----+-----+ 840
ATTTCTCTGCATTTCGTAGGATTGGTTCATATAGGCTCAGTTATGCCTTTTATAGAA

BsaXI
Hin4I
CviJI | BfaI
NlaIV| | EciI |
AciI || |HincII | |
Pfl1108I | || | MjaIV | |
| | || | | | |
ATTTATCGTAGGCGGAGCCTTCGTCAACCTAGATAAGATTATCGCAAAGCGATTGGGGAA
841 -----+-----+-----+-----+-----+-----+ 900
TAAATAGCATCCGCTCGGAAGCAGTTGGATCTATTCTAATAGCGTTTCGCTAACCCCTT

BsaI
DpnI BsmAI
BclI | MnlI|
Sau3AI | Tth111III ||
Hpy188IX | | CjePI | | BccI
| | | | | |
AACTACCATAGGGTTTTCTGATGATCAAGCAGACCTCTCTCAAAAAACCAGAGACCATCT
901 -----+-----+-----+-----+-----+-----+ 960
TTGATGGTATCCCAAAAGACTACTAGTTCGTCTGGAGAGAGTTTTTTGGTCTCTGGTAGA

```

62/111

Figure 16 (Cont.)

```

                                ApoI
                                Tsp509I
                                DpnI
                                Sau3AI
                                Hpy188IX
                                MboII AlwI
                                CjePI      BbsI      MmeI      Hpy188IX
                                |      |      |      |
ACTTGCTAAAGTTGAAACCGAAGACCTGATTGCCTTCGGAATGATCCCTGAATTTGTCGG
961 -----+-----+-----+-----+-----+-----+-----+ 1020
TGAACGATTTCAACTTTGGCTTCTGGACTAACGGAAGCCTTACTAGGGACTTAAACAGCC

                                Bst4CI
                                EarI
                                HinfI      CviRI      SapI      AluI      FokI      AluI      BccI
                                TfiI      MboII      MjaIV      CviJI      MboII      CviJI      FokI
                                |      |      |      |      |      |      |
AAGATTCAACTGCATTGTAAACTGTGAAGAGCTTTCTTTGGATGAGCTTGTAGCCATCCT
1021 -----+-----+-----+-----+-----+-----+-----+ 1080
TTCTAAGTTGACGTAACATTTGACACTTCTCGAAAGAAACCTACTCGAACATCGGTAGGA

                                AluI
                                CjeI      CviJI      MaeII
                                |      |      |
TACAGAACCTACAAATGCGATTGTGAAACAATATATGGAGCTATTCGCAGAAGAAAACGT
1081 -----+-----+-----+-----+-----+-----+-----+ 1140
ATGTCTTGGATGTTTACGCTAACACTTTGTTATATACCTCGATAAGCGTCTTCTTTTGCA

                                MboII
                                BbsI
                                MboII
                                SfcI
                                CviJI      MwoI      CviJI      Cac8I
                                |      |      |      |      |
CAAGTTAGTCTTCAAAAAAGAAGCCCTATATGCTATAGCAAAAAAGCCAAGCAAGCAAA
1141 -----+-----+-----+-----+-----+-----+-----+ 1200
GTTCAATCAGAAGTTTTTTCTTCGGGATATACGATATCGTTTTTTTCGGTTCGTTTCGTTT

```



64/111

Figure 16 (Cont.)

			BbvI			CviRI
			MunI			Fnu4HI
			Tsp509I			AluI
		NlaIII				CviJI
	BslI	Hpy178III				TseI
	EcoNI	RcaI				MwoI

TATTTTAGGGGTGTCATGACAACAATTGCCATAGAAGCTGCAAAAAAAGTTCTTATCAAA  
 1381 -----+-----+-----+-----+-----+-----+ 1440  
 ATAAAATCCCCACAGTACTGTTGTTAACGGTATCTTCGACGTTTTTTTCAAGAATAGTTT

	BsaAI
	SnaBI
	MaeII  CviRI EcoRV
	CTACGTAATGCAGGATATCAGGCATA
1441	-----+-----+-----+-----+-----+ 1466
	GATGCATTACGTCCTATAGTCCGTAT

65/111

**Figure 17. Restriction enzyme analysis of the *C. pneumoniae* CLP protease subunit gene (SEQ ID NO: 13).**

```

                                     Hpy178III
                                     DpnI |
                                     MaeII BfaI Sau3AI | |
                                     AluI |AvrII| Hpy178III | | |
                                     CviJI |BsaJI| Sth132I | | | |
MaeII ||CviJI DdeI | | StyI|SimI | | | |MaeII
| || | | | | | | | | | |
TGACGTAGACAGCCTAAAAAGTCTTAGCTACGTTCTAGGGTCATTTTCGTGATCGGGAAC
1 -----+-----+-----+-----+-----+-----+-----+ 60
ACTGCATCTGTCGGATTTTTCAGAATCGATGCAAGGATCCCAGTAAAGCACTAGCCCTTG

                                     KpnI
                                     BsrI |
                                     NlaIV |
                                     RsaI |
                                     TspRI |
                                     Tsp509I MnlI BaeI BanI | MnlI
                                     | | | | |
GTATGGACACAACCTGAAAATTATTTGATGAGGAAACGCAAATGACACTGGTACCCTATGT
61 -----+-----+-----+-----+-----+-----+-----+ 120
CATACCTGTGTTGACTTTTAATAAACTACTCCTTTGCGTTTACTGTGACCATGGGATACA

                                     EbsI
                                     MboII
                                     Hin4I |
                                     CjeI | |
                                     NlaIII| | |
                                     HphI || | |
                                     BsaJI | || | |
                                     BaeI BsaJI BstDSI | || | |
Sth132I | BstDSI NcoI | || | |
TaqI | CviJI| StyI | || | |
BceFI | | HaeIII| CviJI| | || | | Hpy188IX | |
BciVI | | BscGI || HaeIII| | || | | Sth132I | | |
CjeI | | Sau96I || Sau96I || | || | | BscGI | | | |
| | | | | | | | | | | | | | |
TGTCGAGGATACGGGCCGTGGTGAAAGGGCCATGGATATTTACTCCCGTCTTCTGAAAGA
121 -----+-----+-----+-----+-----+-----+-----+ 180
ACAGCTCCTATGCCCGGCACCACTTTCCCGGTACCTATAAATGAGGGCAGAAGACTTTTCT

                                     BanII Tth111III
                                     Bsp1286I Tsp509I |
                                     CviJI | Bst4CI | |
TaqII Sau3AI | | NlaIV| | MnlI | | |
| | | | | | | | | | |
TCGTATTGTAATGATCGGTCAGGAAATCACGGAGCCCTCGCAAACACAGTAATTGCCCA
181 -----+-----+-----+-----+-----+-----+-----+ 240
AGCATAACATTACTAGCCAGTCCTTTAGTGCCTCGGGGAGCGTTTGTGTCATTAACGGGT

```

66/111

Figure 17 (Cont.)

```

                                DpnI
                                BstYI |
                                Sau3AI |
                                MnlI | |
                                Hpy188IX| | |
                                AlwI | | | |
AluI                                NlaIII| | | |
CviJI    AceIII | | | | | MboII    Tsp509I    Tsp509I    EcoRII |
| | | | | | | | | | | | | | | | | | | | | |
GCTCCTTTTCTCATGTCCGAAGATCCTAAAAAGGATATTCAAATTTTCATCAATTCCCC
241 -----+-----+-----+-----+-----+-----+ 300
CGAGGAAAAGGAGTACAGGCTTCTAGGATTTTCTCTATAAGTTTAAAAGTAGTTAAGGGG

                                BsrI
                                HaeIV |
                                Hin4I |
                                MwoI | |
Fnu4HI | | | | | BspGI | | |
HphI | | | | | MspAII | | | |
TauI | | | | | AciI | | | | |
AciI | | | | | | | | | | |
| | | | | | | | | | | |
AGGCGGCTACATCACCGCTGGACTGGCAATCTATGATACCATTCGCTTTTtaggttGTGA
301 -----+-----+-----+-----+-----+-----+ 360
TCCGCCGATGTAGTGGCGACCTGACCGTTAGATACTATGGTAAGCGAAAAATCCAACACT

                                BanII
                                Bsp1286I
                                CviJI |
                                NlaIV| |
                                SfaNI | | |
                                NlaIII| | | |
                                BsaJI | | | | |
                                BstDSI | | | | |
                                CviRI | | | | |
                                Fnu4HI | | | | |
                                AluI | | | | |
                                FokI    CviJI | | | | |
                                CviRI | TseI | NcoI | | | | | AciI
TaqII BbvI | | SfaNI | | StyI | | | | | MnlI |
| | | | | | | | | | | | | | | |
TGTAATACTACTGCATCGGTCAAGCTGCATCCATGGGAGCCCTCTTATTATCCGCAGG
361 -----+-----+-----+-----+-----+-----+ 420
ACATTTATGGATGACGTAGCCAGTTCGACGTAGGTACCCTCGGGAGAATAATAGGCGTCC

```

67/111

Figure 17 (Cont.)

```

                                     BslI
                                     DpnI
                                     Sau3AI
                                     Hpy178III
                                     BstXI
                                     MnlI
                                     XcmI
                                     HgaI
                                     MaeIII
                                     BceI
                                     EarI
                                     SapI
                                     CviJI
                                     AlwI
                                     CjePI
                                     Tsp45I
                                     AACTAAAGGAAAGCGTCACGCTCTTCCCATAGCCGTATGATGATCCACCAACCTTCTGG
421 -----+-----+-----+-----+-----+-----+-----+-----+ 480
                                     TTGATTTCCCTTTCGCAGTGCAGAGAAGGGGTATCGGCATACTACTAGGTGGTTGGAAGACC

                                     MmeI
                                     Tth111III
                                     ApoI
                                     Tsp509I
                                     AluI
                                     CviJI
                                     MspA1I
                                     PvuII
                                     Fnu4HI
                                     TseI
                                     BbvI
                                     Hpy188IX
                                     FokI
                                     Hin4I
                                     AciI
                                     BpmI
                                     AGGCATTATCGGAACATCCGCAGACATCCAACCTCCAAGCAGCTGAAATTCTAACACTAAA
481 -----+-----+-----+-----+-----+-----+-----+ 540
                                     TCCGTAATAGCCTTGTAGGCGTCTGTAGGTTGAGGTTTCGTCGACTTTAAGATTGTGATTT

                                     BsmI
                                     CviRI
                                     MnlI
                                     Hpy188IX
                                     SfcI
                                     Tsp509I
                                     AAAACACCTTGCCAATATCCTCTCTGAATGCACAGGACAACCTGTAGAAAAATTATAGA
541 -----+-----+-----+-----+-----+-----+-----+ 600
                                     TTTTGTGGAACGGTTATAGGAGAGACTTACGTGTCCTGTTGGACATCTTTTTTAATATCT

                                     MboII
                                     BsaJI
                                     CviJI
                                     NlaIV
                                     BccI
                                     HinfI
                                     TfiI
                                     MnlI
                                     NlaIII
                                     MwoI
                                     AGATTCTGAACGAGATTTCTTCATGGGAGCCGAGGAAGCCATCTCCTACGGACTTATTGA
601 -----+-----+-----+-----+-----+-----+-----+ 660
                                     TCTAAGACTTGCTCTAAAGAAGTACCCTCGGCTCCTTCGGTAGAGGATGCCTGAATAACT

                                     MaeIII
                                     BciVI
                                     DdeI
                                     NdeI
                                     TAAGGTGGTAACTTCTGCGAAAGAACTAATAAGGATACAAGTAGCACTTAGAGAGAACA
661 -----+-----+-----+-----+-----+-----+-----+ 720
                                     ATTCACCATTTGAAGACGCTTTCTTTGATTATTCCTATGTTTCATCGTGAATCTCTCTTGT

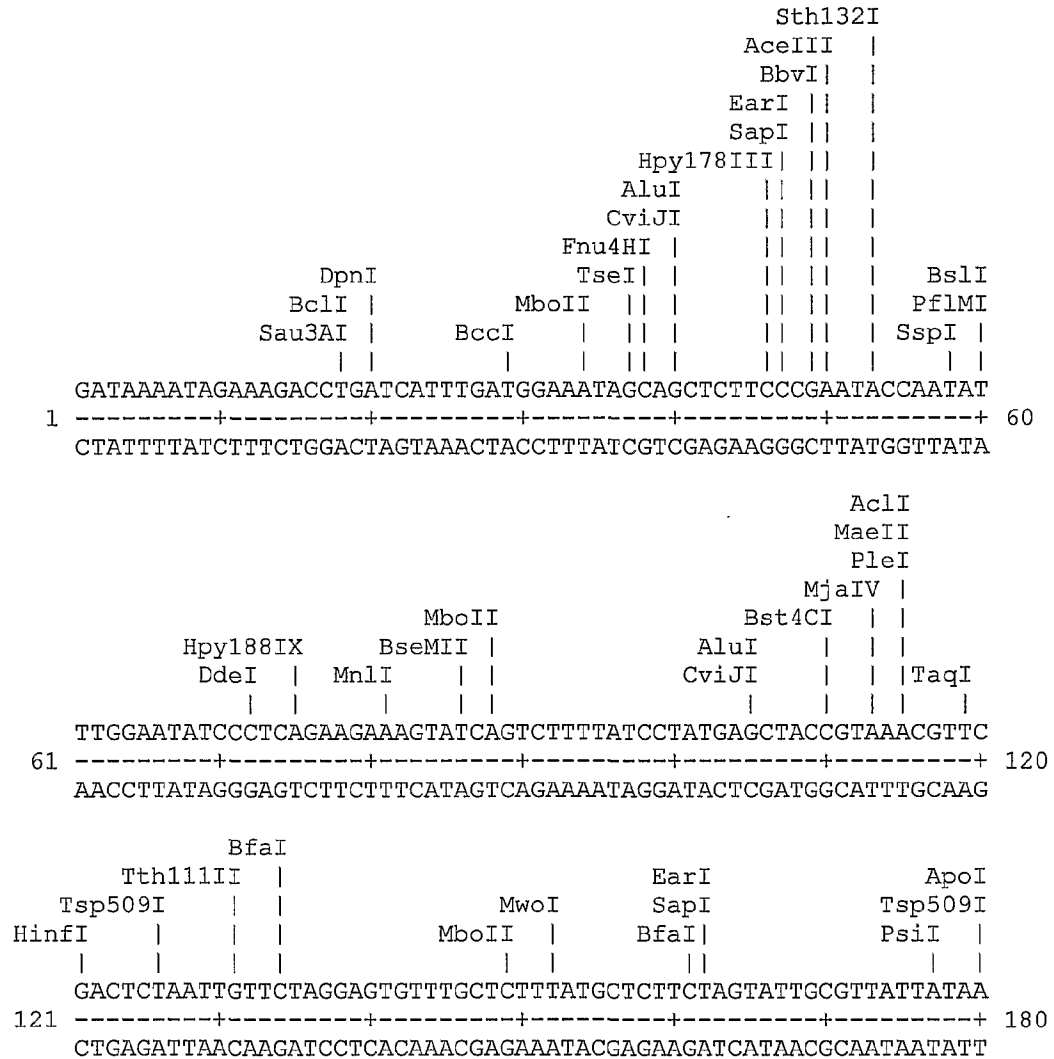
```





69/111

**Figure 18. Restriction enzyme analysis of the *C. pneumoniae* transglycolase/transpeptidase gene (SEQ ID NO: 15).**



70/111

Figure 18 (Cont.)

```

                                AvaI
                                AluI |
                                CviJI |
                                MwoI | |
                                Sth132I| | |
                                AciI  || | |
                                Fnu4HI || | |
                                TauI  || | |
                                BsrI  || | |
                                CviJI || | |
                                HaeIII|| | |
                                TspRI || | |
                                ApoI   Tsp509I
                                ApoI  BsaI   Sau96I || | | | |
                                Tsp509I BsmAI BmrI || | | | |
                                |         | | | | | |
                                AATTCAAATTTGTGAAGGAGACCACTGGGCCGCAGAAGCTCTCGGGCAACACGAATTTTG
181 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 240
                                TTAAGTTTAAACACTTCCTCTGGTGACCCGGCGTCTTCGAGAGCCCGTTGTGCTTAAAC

                                Eco57I
                                BsmAI |
                                BsaAI | |
                                BseSI  Bsp1286I
                                NlaIV|  MaeII|| |
                                DpnI    Sau3AI |  NspV  BmgI||  RsaI||| |
                                AlwI    | |  TaqI  BanI|||  Bst4CI ||| |
                                |        | |  |    |||    | ||| |
                                TGTCCGTGATCCTTTTCGAAGGGGCACCTTTTTTGCTAACACGACAGTACGTAAGGGAGA
241 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 300
                                ACAGGCACTAGGAAAAGCTTCCCCGTGGAAAAACGATTGTGCTGTCATGCATTCCCTCT

                                DpnI
                                BstYI |
                                Sau3AI |
                                CviJI  ApoI   CviRI | |
                                Fnu4HI |  TaqI  Tsp509I  AlwI  | | |
                                TseI  |  BbvI  HphI  |  MslI  | | | |
                                || |  | |  | |  | |  | | | |
                                CAAAGACCTTCAGCAGCCTTTTCGCTGTCGATATTACAAAATTTACACCTTTGTGCAGATCC
301 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 360
                                GTTTCCTGGAAGTCGTCGGAAAGCGACAGCTATAATGTTTTAAAGTGGAACACGTCTAGG

```

71/111

Figure 18 (Cont.)

```

                                MslI
                                Hpy178III|
                                FokI  ||
                                Sth132I |  ||
                                BsgI    |  ||  ||
                                Hpy178III|  |  ||
                                AluI    ||  |  ||  ||
                                CviJI    ||  |  ||  ||  ||
                                |        ||  |  ||  ||
                                TTTAGCTATTCCCGAATGTCATCGTGATGAGATCATCCAAGGGATTCTCCAATTTATTGA
361 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 420
                                AAATCGATAAGGGCTTACAGTAGCACTACTCTAGTAGGTTCCCTAAGAGGTTAAATAACT

                                BsaXI      HaeIV      AluI
                                Pfl1108I  Hin4I|      MnlI      Hin4I      CviJI
                                |          ||          |          |          |
                                GGGGCAGACCTACGACGACCTCTCCCTAAAGTTAGATAAGAAATCTCGGTATTGTAAGCT
421 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 480
                                CCGCGTCTGGATGCTGCTGGAGAGGGATTCAATCTATTCTTTAGAGCCATAACATTCTGA

                                CviJI
                                HaeIV|
                                Hin4I|
                                MspI  ||
                                BsrFI| ||
                                BciVI      NlaIII||  ||      BslI      CviRI
                                |          |||  ||          |          |
                                GTATCCTTTATTAGATGTTTCTGTCCATGACCGGCTATCCCTTTGGTGGAAGGATATGC
481 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 540
                                CATAGGAAATAATCTACAAAGACAGGTAAGGCGGATAGGGAACACCTTTCCTATACG

                                BaeI
                                SfaNI      CjeI|
                                |          ||
                                AACAAAGCATCGCTTACCAACAAACGCCCTATTTTTTATTACGGACTACCAACGCTCGTA
541 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 600
                                TTGTTTCGTAGCGAATGGTTGTTTGCGGGATAAAAAATAATGCCTGATGGTTGCGAGCAT

                                BsaJI
                                StyI
                                BaeI  |
                                CjeI  |
                                AluI  |
                                CviJI|  |
                                CjePI  BciVI  ||  |      BsaXI      SmlI|      MseI
                                |        ||  |      |          |          |
                                TCCTTTTGGGAAGCTCCTTGGACAAGTTCTCCATACCTTAAGAGAAATTAAGGATGAGAA
601 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 660
                                AGGAAAACCTTCGAGGAACCTGTTCAAGAGGTATGGAATTCCTTTAATTCCTACTCTT

```

72/111

Figure 18 (Cont.)

```

                                MnlI
                                XcmI
                                FauI  AciI|
                                Sth132I| BslI|
                                FokI CviJI || BslI| BccI |RsaI | MseI | Hpy178III
                                | | | | | | | |
AACAGGAAAAGCCTTTCCACAGGCGGGATGGAGGCGTACTTTAATCATATTCTGGAAGG
661 -----+-----+-----+-----+-----+-----+-----+ 720
TTGTCCTTTTCGGAAAGGGTGTCCGCCCTACCTCCGCATGAAATTAGTATAAGACCTTCC

                                AluI
                                CviJI
MaeII BsmFI | Bst4CI HinfI
| | | | TfiI
| | | | BsaBI|
GGACGTTGGAGAGAGAAAGCTGTTGCGTTCTCCTTTGAACCGTTTAGATACGAATCGTGT
721 -----+-----+-----+-----+-----+-----+ 780
CCTGCAACCTCTCTCTTTGACAACGCAAGAGGAACTTGGCAAATCTATGCTTAGCACA

                                EcoRV
                                Hpy188IX |
                                CviJI | |
                                BccI | | |
                                BslI | | | |
                                | | | |
TATCAAAGTGCCTAAAGATGGCTCTGATATCTACCTTACGATCAATCCTGTGATCCAGAC
781 -----+-----+-----+-----+-----+-----+ 840
ATAGTTTGACGGATTTCTACCGAGACTATAGATGGAATGCTAGTTAGGACACTAGGTCTG

                                ScrFI
                                BsaJI|
                                BsaJI||
CviRI TaqI BscGI BfaI AluI EcoRII||
MnlI | Sth132I |MboII|Cac8I | CviJI CviJI||| CviJI
| | | | | | | |
CATTCAGAGGAAGAACTCGAACGGGGCGTGCTAGAAAGCTAAAGCCCAGGGGGGTAGGCT
841 -----+-----+-----+-----+-----+-----+ 900
GTAACGTCTCCTTCTTGAGCTTGCCCCGCACGATCTTCGATTCGGGTCCCCCATCCGA

                                CviRI
                                Tth111III | BsrI
                                HinfI | | TspRI
                                MslI TfiI | | CviJI| AlwI | | |
                                | | | | |
CATTCATTAATGAAGTCCCAAACAGGAGAGATTCTTGCACTGGCTCAATATCCGTTTTTCGA
901 -----+-----+-----+-----+-----+-----+ 960
GTAAGATTACTTGAGGGTTTGTCTCTCTAAGAACGTGACCGAGTTATAGGCAAAAAGCT

```

73/111

Figure 18 (Cont.)

```

                                TaqI
                                BaeI |
                                HhaI | SfaNI
Tsp509I PsiI RleAI
| | |
TCCCACAAATTATAAGGAATACTTCAATAACAAAGAGCGCATCGAACATACGAAGGTATC
961 -----+-----+-----+-----+-----+-----+ 1020
AGGGTGTTTAATATTCCTTATGAAGTTATTGTTTCTCGCGTAGCTTGTATGCTTCCATAG

                                NlaIII
                                Hpy178III |
                                RcaI | |
                                DpnI | | |
                                Sau3AI | | | |
                                Sth132I | | | |
                                TaqI | | | |
                                SimI | | | | |
                                NciI | | | | |
                                ScrFI | | | | |
                                SmaI | | | | |
                                MspI | | | | |
                                NciI | | | | |
                                ScrFI | | | | |
                                Sth132I | | | | |
                                BaeI | BsaJI | | | | | Bst4CI
                                | | | | | |
TTTTGTGAGCGATGTTTTTGAACCCGGGTCGATCATGAAACCTTTGACTGTGGCGATTGC
1021 -----+-----+-----+-----+-----+-----+ 1080
AAAACACTCGCTACAAAACTTGGGCCAGCTAGTACTTTGGAACTGACACCGCTAACG

                                MboII
                                MseI
                                AluI |
                                MnlI CviJI |
                                EarI | Cac8I | |
                                AluI | | BfaI | | |
                                CviJI | | CviJI | | |
                                MwoI | | | NheI | | | |
                                | | | | | |
TTTACAAGCTAACGAAGAGGCTAGCTTAAATCGCAGAAAAAGATTTTTGATCCTGAAGA
1081 -----+-----+-----+-----+-----+-----+ 1140
AAATGTTTCGATTGCTTCTCCGATCGAATTTTAGCGTCTTTTCTAAAACTAGGACTTCT

```

74/111

Figure 18 (Cont.)

```

                MboII
                ScrFI
                Eco57I|
                EcoRII||
                MaeIII  |||
                Tsp45I  |||
                MboII  |  |||
                ClaI   |  |||
                TaqI   |  |||
                |  |  |  |||
                ACCTATCGATGTGACCAGGACACTCTTCCCTGGACGAAAAGGATCTCCGCTTAAGGATAT
1141 -----+-----+-----+-----+-----+-----+-----+ 1200
                TGGATAGCTACACTGGTCCTGTGAGAAGGGACCTGCTTTTCTAGAGGCGAATTCCTATA

                                Hpy178III
                                MboII|
                                CviJI  ||
                                NlaIII|  ||
                                CjePI  ||  ||
                                RsaI   |  ||  ||
                BfaI                MunI   BsrGI |  |  |  ||
Hpy178III                XbaI|      Tsp509I  TatI |  |  |  ||
                ||                |  |  |  ||  ||
                TTCTAGAAACTCTCAATTGAATATGTACATGGCTATCCAGAAATCTTCGAATGTCTATGT
1201 -----+-----+-----+-----+-----+-----+-----+ 1260
                AAGATCTTTGAGAGTTAACTTATACATGTACCGATAGGTCTTTAGAAGCTTACAGATACA

                                CviJI
                                Cac8I |
                                MwoI|  |
                                AluI||  |
                                CviJI||  |
                                MspAII||  |
                                PvuII||  |
                Bpu1102I  |||  |
                DdeI     |||  |
                AluI     |||  |
                CjePI    |||  |BseMII
                CviJI    |||  |AciI|      SfaNI
                ||  |||  |  ||
                AGCTCAGCTGGCTGACCGCATCATACAATCTTTAGGAGTGGCCTGGTACCAACAGAAGTT
1261 -----+-----+-----+-----+-----+-----+-----+ 1320
                TCGAGTCGACCGACTGGCGTAGTATGTTAGAAATCCTCACCGGACCATGGTTGTCTTCAA

                                KpnI
                                NlaIV |
                                RsaI  |
                                BanI  |  |
                                ScrFI  |  |  |
                                CviJI  |  |  |
                                EcoRII |  |  |
                                HaeI   |  |  |
                                HaeIII |  |  |
                                CjeI   |  |  |
                                ||  |  |  |
                AGCTCAGCTGGCTGACCGCATCATACAATCTTTAGGAGTGGCCTGGTACCAACAGAAGTT
1261 -----+-----+-----+-----+-----+-----+-----+ 1320
                TCGAGTCGACCGACTGGCGTAGTATGTTAGAAATCCTCACCGGACCATGGTTGTCTTCAA

```

75/111

Figure 18 (Cont.)

```

                                BmrI
                                BsrI|
                                MnlI ||
                                AlwI | ||
                                AluI| | ||
                                CviJI| | || CviJI
                                TaqI  || | || HaeI
                                DpnI|  || | || HaeIII
                                MboII ||  || | || StuI
                                Sau3AI ||  || | || TspRI|
                                ||| |  || | || ||
GCTAGCTCTGGGATTTGGAAGAAAAACAGGGATCGAGCTTCCCAGTGAGCCTCTGGTTT
1321 -----+-----+-----+-----+-----+ 1380
CGATCGAGACCCTAAACCTTCTTTTGTCCCTAGCTCGAAGGGTCACTCCGGAGACCAA

                                ScrFI
                                BsaJI |
                                EcoRII |
                                NlaIV  | |
                                DrdII| | |
                                BstXI  || | |
                                NlaIV  || | | AvaII
                                BanI  |  || | | Sau96I
                                MnlI  |  || | | BslI  |
                                |  |  || | | |
GGTGCCTTCTCCCATCGTTTCCATATTAATGGTTCCTGGAATGGTCCTTATCTACTCC
1381 -----+-----+-----+-----+-----+ 1440
CCACGGAAGAGGGGTAGCAAAGGTATAATTACCAAGGGACCTTACCAGGAATAGATGAGG

                                CviJI      SspI  BciVI      DrdII CviJI
                                |          |          |          |
ATATTCTTTGGCTATGGGATATAATATTTTGGCAACAGGGATACAAATGGTTCAAGCCTA
1441 -----+-----+-----+-----+-----+ 1500
TATAAGAAACCGATACCCTATATTATAAAACCGTTGTCCCTATGTTTACCAAGTTCGGAT

                                Bcefi      CviJI
                                CviRI|      HaeIII
                                MnlI|      Sau96I|
                                MwoI  ||      MspI  ||      Sau3AI  |
                                |  ||      |  ||      Eco57I  |
CGCTATCCTTGCAAACGGAGGTTATGCCGTCCGGCCCACTTTAGTAAAAAAGATCGTCTC
1501 -----+-----+-----+-----+-----+ 1560
GCGATAGGAACGTTTGCTCCAATACGGCAGGCCGGGTGAAATCATTTTTTCTAGCAGAG

```

Figure 18 (Cont.)

	Hpy178III						Tsp509I		
	MnlII						Hpy188IX		
BsmAI						MboII			
BsmBI		MboII			PleI	BbsI			
	}								
	TGCTTCAGGAGAGGAATATCATCTTCCCTACTAAAGAGAAGACACGACTCTTTTCAGAAGA								
1561	-----+-----+-----+-----+-----+								1620
	ACGAAGTCCTCTCCTTATAGTAGAAGGATGATTCTCTTCTGTGCTGAGAAAAGTCTTTCT								
							Hpy178III		
							Sth132I		
						MspI			
						NciI			
						ScrFI			
						Sth132I			
					MnlI				
	MboII	XmnI			MaeIII				
	BfaI	PpiI		NlaIII	AclI				
					MaeII				
	AATTACTAGAGAAGTTGTTTCGTGCCATGCGTTTTACAACGTTACCCGGAGGTTCTGGGATT								
1621	-----+-----+-----+-----+-----+								1680
	TTAATGATCTCTTCAACAAGCACGGTACGC AAAATGTTGCAATGGGCCTCCAAGCCCTAA								
			MnlI	SfaNI					
CviJI	Bpu10I		BfaI			CjePI	HinfI		
TaqI		DdeI		MslI		SfcI	TfiI		
	TCGAGCCTCTCCTTAAGCATCACTCTAGTGCTGGGAAAAACAGGAACTACAGAAAAGATGAT								
1681	-----+-----+-----+-----+-----+								1740
	AGCTCGGAGAGGATT CGTAGTGAGATCACGACCCTTTTGT CCTTGATGTCTTTTCTACTA								
							Sth132I		
BceFI	NlaIII	CjePI				BscGI			
	TCATGGAAAATATGATAAACGCCGTCATATTGCTTCTTTTATAGGTTTTACTCCCGTAGA								
1741	-----+-----+-----+-----+-----+								1800
	AGTACCTTTTATACTATTTGCGGCAGTATAACGAAGAAAATATCCAAAATGAGGGCATCT								



77/111

Figure 18 (Cont.)

```

      ApoI
      Tsp509I
Hpy188IX |
BanII | |
BsiHKAI | |
Bsp1286I | |
SacI | |
AluI | |
CviJI | |
MnlI | | | CjeI | SfaNI | CjePI | BsmBI | | | BslI |
| | | | | | | | | | | | | | | |
GAGCTCGGAGGGAAATTTCCACCTTTAGTGATGCTCGTCTCCATAGATGATCCTGAATA
1801 -----+-----+-----+-----+-----+-----+-----+ 1860
CTCGAGCCTCCCTTTAAAGGGTGGAAATCACTACGAGCAGAGGTATCTACTAGGACTTAT

      NlaIV
      BanI |
      Fnu4HI | |
      TauI | |
      CviJI | |
      Cac8I | |
      CjePI | | Tsp509I BceI |
      | | | | | | |
TGGTTTGGGACCGACGGCACGAAAAATTATATGGGGGGGCGTTGTGCGGCACCCATTTT
1861 -----+-----+-----+-----+-----+-----+-----+ 1920
ACCAAACGCTCGGCTGCCGTGCTTTTTTAATATACCCCCCGCAACACGCCGTGGGTAAAA

      Hpy178III
      HinfI | BcgI
      TfiI | DdeI |
      MnlI | | AluI | |
      BfaI | BseRI | MboII | | CviJI | |
      | | | | | | |
TTCTAGGGTTGCTGACCGCACACTCCTCTATTTAGGGATTCTTCCAGACAAGAAGCTAAG
1921 -----+-----+-----+-----+-----+-----+-----+ 1980
AAGATCCCAACGACTGGCGTGTGAGGAGATAAATCCCTAAGAAGGTCTGTTCTTCGATTC

      MseI
      CviRI |
      MboII |
      Fnu4HI | |
      HgaI | |
      TseI | | |
      Fnu4HI | | | |
      BbvI | AluI | | | | BsmAI | MboII | |
      BbvI | CviJI | | | | BsmBI | HinfI | | |
Tsp509I | | TseI | | | | BcgI | TfiI | | | |
| | | | | | | | | | | | |
AAATTGCGACGAAGAAGCTGCTGCATTAAAGCGTCTCTATGAAGAATGGAATCGTTCTCC
1981 -----+-----+-----+-----+-----+-----+-----+ 2040
TTTAACGCTGCTTCTTCGACGACGTAATTTTCGAGAGATACTTCTTACCTTAGCAAGAGG

```

78/111

Figure 18 (Cont.)

```

                                DpnI
                                BstYI | AlwI
                                BslI | MnlI Sau3AI | HphI | BccI SfcI Bst4CI
                                | | | | | | | |
2041 -----+-----+-----+-----+-----+-----+-----+ 2100
                                GAAACAAGGGGGAACGAGGTGAGGATCTCTATTTCCATCTTGCTATAGACTTTTACCGTT
                                CTTTGTTCCCCCTTGCTCCACTCCTAGAGATAAAGGTAGAACGATATCTGAAAATGGCAA

                                BsmAI
                                BsmBI
                                Sth132I|
                                BanII ||
                                BscGI ||
                                Bsp1286I ||
                                Hin4I ||
                                CviJI | ||
                                Hin4I | ||
                                BseRI | | ||
                                Hpy188IX | | | ||
                                HaeIV | | | | ||
                                Hin4I | | | | ||
                                PleI HinfI | | | | | || BplI MnlI MnlI
                                | | | | | | | | | |
2101 -----+-----+-----+-----+-----+-----+-----+ 2160
                                GAGCAAAGACTCTCTATCAGAGAGCCCGTCTCCTCTTTATCCTCTATGAGTAGTTTATGT
                                CTCGTTTCTGAGAGATAGTCTCTCGGGCAGAGGAGAAATAGGAGATACTCATCAAATACA

                                TA
2161 -- 2162
                                AT

```

79/111

**Figure 19. Restriction enzyme analysis of the *C. pneumoniae* CLPc protease gene (SEQ ID NO: 17).**

```

                                ApoI
                                Tsp509I
                                DraI|
                                MboII  MseI||
                                CviRI  |SfaNI |||
ApoI      ApoI      EarI      MboII  MseI|||
Tsp509I    Tsp509I
|          |          |          |  |  |  |  |
GAATTTTACCAAATTTGCTGGTTTAGAGCGAAGAGTTGCATCATTATTTTAAATTTTCGTA
1  -----+-----+-----+-----+-----+-----+ 60
CTTAAATGGTTTAAACGACCAAATCTCGCTTCTCAACGTAGTAATAAAATTTAAAGCAT

                                MseI
                                AflIII|
                                SmlI|          Tth111III          MjaIV
                                ||          |          |
TATGCTTAAAGGAAAGTTCTACCCCTGTCTTTTAGGTTTTTATGTTTGAGAAGTTCACTAA
61 -----+-----+-----+-----+-----+-----+ 120
ATACGAATTCCTTTCAAGATGGGGACAGAAAATCCAAAAATACAACTCTTCAAGTGATT

                                Bpu1102I      BseMII
                                MnlI      DdeI      DraI  | BseMII
                                BsrI|      CviJI|      MseI|  | EcoRII
                                |          ||          ||          |
TAGAGCAAAACAAGTCATTAAACTGGCGAAAAAGGAGGCTCAGCGTTTAAATCATACTA
121 -----+-----+-----+-----+-----+-----+ 180
ATCTCGTTTTGTTTCAGTAATTTGACCGCTTTTTCCTCCGAGTCGCAAATTTAGTATTGAT

                                BbsI
                                MboII
                                BstAPI|
                                BsiHKAI  ||
                                Bsp1286I  ||
FokI  Tth111III  |  ||          MseI
ScrFI  DdeI  |  |  ||          AluI  |
BsaJI|  RsaI  |  |  |MwoI|          CviJI  |
||  |  |  |  |  ||          |  |
CCTGGGTACTGAGCACATCCTGCTTGGTCTTCTCAAACCTGGTCAAGGGGTAGCTGTTAA
181 -----+-----+-----+-----+-----+-----+ 240
GGACCCATGACTCGTGTAGGACGAACCAGAAGAGTTTGAACCAGTTCCCCATCGACAATT

                                BcefI
                                CjePI  |
                                BsaJI  MnlI      MnlI      BcefI|  |
                                |          |          |          ||  |
TGTATTACGCAACCTCGGTATAGATTTTGATACGGCACGGCAAGAGGTGGAACGCCTGAT
241 -----+-----+-----+-----+-----+-----+ 300
ACATAATGCGTTGGAGCCATATCTAAACTATGCCGTGCCGTCTCCACCTTGCGGACTA

```

80/111

Figure 19 (Cont.)

```

      ApoI
      Tsp509I      MjaIV
      BspGI |      AccI|
      Hpy178III |      BsaI|
      AvaII | |      BsmAI|
      Sau96I | |      CjePI ||      SimI      EarI      MboII
      | | |      | ||      |      |      |
301  TGGTTATGGTCCAGAAATTCAGTCTACGGAGACCCTGCCCTTACAGGAAGAGTAAAAAA
-----+-----+-----+-----+-----+-----+ 360
      ACCAATACCAGGTCTTTAAGTTCAGATGCCTCTGGGACGGGAATGTCCTTCTCATTTTTT

      MboII      Hpy178III
      CviJI |      MslI |
      Cac8I | |      Sth132I |
      CviJI | | |      Tsp509I |
      HinfI      MnlI      HaeI | | |      BsiHKAI| |
      TfiI      EarI|      HaeIII | | |      Bsp1286I| |
      | |      | | |      | | |      | | |
361  ATCTTTTGAATCAGCAAATGAAGAGGCCAGCCTTTTAGAGCACAATTATGTCGGGACGGA
-----+-----+-----+-----+-----+ 420
      TAGAAAACCTTAGTCGTTTACTTCTCCGGTCGGAAAATCTCGTGTTAATACAGCCCTGCCT

      AlwI
      HaeIV |
      Hin4I |
      DpnI | |
      NlaIV | |
      BamHI | | |
      BstYI | | |
      Sau3AI | | |
      AlwI | | |      MboII
      DdeI | | | |      Hpy188IX |      EarI
      BsmFI | | | |      Eco57I | |      SapI
      | | | |      | | |      |
421  GCATTTACTCTTAGGGATCCTACATCAATCAGATAGTGTGCTCTTCAGGTATTAGAAAA
-----+-----+-----+-----+-----+ 480
      CGTAAATGAGAATCCCTAGGATGTAGTTAGTCTATCACAGCGAGAAGTCCATAATCTTTT

      MnlI
      DpnI|
      Sau3AI ||
      ClaI| ||
      TaqI| ||
      AlwI || ||
      CjeI || ||
      | || ||
481  CTTACATATCGATCCAAGAGAGGTTTCGTAAGGAAATCTTAGAGAATTAGAGACCTTCAA
-----+-----+-----+-----+-----+ 540
      GAATGTATAGCTAGGTTCTCTCCAAGCATTCCTTTAAGAATCTCTTAATCTCTGGAAGTT

```

81/111

Figure 19 (Cont.)

```

          FokI
        MboII|
          MnlI|
        BbsI  ||
        MboII ||
          |  ||
TCTACAACTTCCTCCTTCGTCGTCGTCCTTCTTCCTCATCCTCTCGAAGCAACCCTTCATC
541 -----+-----+-----+-----+-----+-----+ 600
AGATGTTGAAGGAGGAAGCAGCAGCAGAAGAAGGAGTAGGAGAGCTTCGTTGGGAAGTAG

          Bpu10I
          DdeI
          AluI|
        CviJI| Hpy188IX
          ||      |
TTCAAAATCTCCTTTAGGTCATAGCTTAGGTTCTGACAAAACGAAAAGCTTTCTGCTCT
601 -----+-----+-----+-----+-----+-----+ 660
AAGTTTGTAGAGGAAATCCAGTATCGAATCCAAGACTGTTTTTGCTTTTCGAAAGACGAGA

          Eco57I
          DpnI |
          Sau3AI | |
          HinfI
          Hpy188IX |
          AvaII  | |
          Sau96I  | |
          CjePI   | | |
MwoI NdeI      MseI | BccI| | |DdeI | | | | | MboII
|      |      |      | | | | | | | | | | | BslI|
GAAAGCATATGGTTATGATTTAACGGAGATGGTCCGAGAGTCTAAGCTCGATCCTGTTCAT
661 -----+-----+-----+-----+-----+-----+ 720
CTTTCGTATACCAATACTAAATTGCCTCTACCAGGCTCTCAGATTCGAGCTAGGACAGTA

          Bst4CI
          Hpy188IX TaqI |
          |      |      |
TGGTCGTTCTTCAGAAGTCGAACGGTTGATTTTGATTCTTTGCCGAAGAAGAAAAACAA
721 -----+-----+-----+-----+-----+-----+ 780
ACCAGCAAGAAGTCTTCAGCTTGCCAACTAAACTAAGAAACGGCTTCTTCTTTTTTGT

          BpmI
          MnlI |
          MunI | |
          RsaI
          TatI |
          |      |
          AluI
          CviJI
          Tsp509I| |
          CviRI|| |
          SimI CviJI
          |      |
TCCTGTACTIONTATTGGAGAAGCTGGAGTTGGTAAGACTGCAATTGTTGAGGGTCTGGCTCA
781 -----+-----+-----+-----+-----+-----+ 840
AGGACATGAATAACCTCTTCGACCTCAACCATTCTGACGTTAACAACTCCCAGACCGAGT

```

82/111

Figure 19 (Cont.)

```

                                     DpnI
                                     BglIII |
                                     BstYI |
                                     Sau3AI |
                                     BfaI | |
                                     Hpy178III | |
                                     XbaI | | |
                                     | | | |
AAAATCATTTCTGAATGAGGTTCTGATGCCTTACGGAAAAAGCGACTGATTACTCTAGA
841 -----+-----+-----+-----+-----+-----+ 900
TTTTTAGTAAGACTTACTCCAAGGACTACGGAATGCCTTTTTCGCTGACTAATGAGATCT

                                     AluI
                                     DpnI AlwI
MseI Tsp509I
BfaI VspI MnlI TaqI MnlI| Sau3AI | CviJI
| | | | | | |
TCTAGCATTAAATGATTGCTGGAACAAAATATCGAGGGCAATTTGAGGAACGGATCAAAGC
901 -----+-----+-----+-----+-----+ 960
AGATCGTAATTACTAACGACCTTGTTTTATAGCTCCCGTTAAACTCCTTGCCTAGTTTCG

                                     BanII
                                     BsiHKAII
                                     Bsp1286I
                                     SacI
NlaIII
Cac8I | Tth111III EarI AluI |
NlaIII FokI | MboII | SapI CviJI |
| | | | | |
TGTCATGGATGAAGTTCGCAAGCATGGAACATCTTGCTCTTCATTGACGAGCTCCACAC
961 -----+-----+-----+-----+-----+ 1020
ACAGTACCTACTTCAAGCGTTTCGTACCTTTGTAGAACGAGAAGTAACTGCTCGAGGTGTG

                                     AluI
                                     CviJI
                                     MspAII
                                     PvuII
Fnu4HI | BbvI MwoI Tth111III
MwoI | MwoI | ClaI | DraI |
TseI | SfaNI | TaqI | Eco57I MseI |
| | | | | |
GATTGTAGGAGCAGGAGCAGCTGAAGGTGCTATCGATGCTTCAAACATTTTAAAACCTGC
1021 -----+-----+-----+-----+-----+ 1080
CTAACATCCTCGTCCTCGTCGACTTCCACGATAGCTACGAAGTTTGTAATAATTTTGGACG

                                     HhaI
                                     ThaI
BspMI | ApoI TspRI
MnlI | Tsp509I HphI | Pfl1108I BsaBI Cac8I
| | | | | |
GTTAGCGCGAGGTGAAATTCAGTGTATTGGAGCAACTACGATAGATGAGTATCGCAAGCA
1081 -----+-----+-----+-----+-----+ 1140
CAATCGCGCTCCACTTTAAGTCACATAACCTCGTTGATGCTATCTACTCATAGCGTTTCGT

```

83/111

Figure 19 (Cont.)

```

                                HgaI
                                AluI |
                                CviJI |
                                Fnu4HI | | AloI
                                TseI | | BbvI |
                                Tth111II | | | MaeII | |
                                | | | | |
CATAGAAAAAAGACGCAGCTTTAGAACGTCGTTTCCAAAAAATCGTGGTTCACCCCTCCTAG
1141 -----+-----+-----+-----+-----+-----+ 1200
GTATCTTTTTCTGCGTCGAAATCTTGCAGCAAAGGTTTTTTAGCACCAAGTGGGAGGATC

                                Hpy178III
                                SmlI |
                                CviJI | |
                                HaeI | |
                                HaeIII | |
                                MnlI
                                BsmAI | CjePI Bce83I MaeII | | | CjePI BbsI | |
                                || | | | | | | | | | | MboII | |
                                | | | | | | | | | | |
TGTAGATGAGACTATTGAGATTTTACGTGGCCTCAAGAAAAAGTATGAAGAACATCACAA
1201 -----+-----+-----+-----+-----+-----+ 1260
ACATCTACTCTGATAACTCTAAAATGCACCGGAGTTCTTTTTCATACTTCTTGTAGTGT

                                HinfI
                                Eco57I |
                                Fnu4HI |
                                AluI | |
                                CviJI | |
                                MspAII | |
                                PvuII | |
                                TseI | |
                                P1eI | |
                                Fnu4HI | | |
                                TseI | | | |
                                MboII | | | |
                                MwoI | | | |
                                DraI | | | |
                                MseI | | | |
                                AluI | | | | |
                                CviJI | | | | |
                                BbvI | | | | |
                                HindIII | | | | |
                                || | | | | |
TGTCTTCATTACTGAAGAAGCTTTAAAAGCAGCTGCGACTCTTTCTGATCAATATGTTCA
1261 -----+-----+-----+-----+-----+-----+ 1320
ACAGAAGTAATGACTTCTTCGAAATTTTCGTCGACGCTGAGAAAGACTAGTTATACAAGT

```

84/111

Figure 19 (Cont.)

```

      BsaXI      DpnI      BanII
      Hin4I|      BglIII|      Bsp1286I
      MaeII ||      BstYI|      AluI BssSI|
      NlaIII | ||      MnlI Sau3AI |      CviJI CviJI||
      | | ||      | | |      | | |
      TGGACGTTTCCTCCCTGATAAAGCAATAGATCTTTTAGATGAAGCTGGGGCTCGTGTCGG
1321 -----+-----+-----+-----+-----+-----+-----+ 1380
      ACCTGCAAAGGAGGGACTATTTTCGTTATCTAGAAAATCTACTTCGACCCCGAGCACAGGC

      SfcI      BfaI
      CviJI |      AluI|
      SimI | |      MseI MnlI || CviJI TaqI
      | | |      | | |      | | |
      TGTGAATACAATGGGTCAGCCTACAGATTTAATGAAGCTAGAGGCTGAAATCGAAAATAC
1381 -----+-----+-----+-----+-----+-----+-----+ 1440
      ACAC'TTATGTTACCCAGTCGGATGTCTAAATTACTTCGATCTCCGACTTTAGCTTTTATG

      EarI
      BsaAI|
      MaeII||
      MjaIV |||
      PstI | |||
      CviRI | | |||
      Fnu4HI | | | |||
      CviJI CviJI      SfcI | | | |||
      HaeI HaeI      AluI| | | | |||
      HaeIII HaeIII      CviJI| | | | |||
      MscI Cac8I | Hpy178III | TseI| | | | |||
      EaeI | Bce83I | | SmlI | | CjePI|| | | | |||
Tsp509I | | CjePI | | | BcgI| | | BspMI | | | | |||
      | | | | | | | | | | | | | | | | | |
      AAAATTGGCCAAAGAGCAGGCCATTGGAAGTCAAGAATACGAAAAAGCTGCAGGTTTACG
1441 -----+-----+-----+-----+-----+-----+-----+ 1500
      TTTTAACCGGTTTCTCGTCCGGTAACCTTGAGTTCTTATGCTTTTTTCGACGTCCAAATGC

      MaeII
      NruI |
      ThaI |
      Hpy178III| |
      BcgI MboII || | CviRI      EarI
      | | | | | | |      SapI
      | | | | | | |
      TGATGAAGAGAAAAAAGCTTCGCGAACGTCTGCAAAGTATGAAACAGGAATGGGAAAAATCA
1501 -----+-----+-----+-----+-----+-----+-----+ 1560
      ACTACTTCTCTTTTTTGAAGCGCTGCAGACGTTTCATACTTTGTCCTTACCCTTTTAGT

```



85/111

Figure 19 (Cont.)

MboII  
 BsiHKAI |  
 Bsp1286I | SfcI  
 | |  
 TAAAGAAGAGCACCAAGTTCCTGTAGATGAAGAAGCAGTCGCTCAGGTAGTTTCTCTACA  
 1561 -----+-----+-----+-----+-----+-----+ 1620  
 ATTTCTTCTCGTGGTTCAAGGACATCTACTTCTTCGTCAGCGAGTCCATCAAAGAGATGT  
 BseMII  
 CviJI |  
 BslI | |  
 EcoNI | | |  
 Tth111III | | |  
 ApoI BbvCI | | | | AluI  
 EcoRI Bpu10I | | | | AlwNI  
 Tsp509I DdeI | | | MnlI | CviJI Hpy188IX  
 | | | | | |  
 AACAGGAATTCCTCAGCAAGGCTCACAGAAGCTGAAAGTGAGAAGCTTCTGAAGTTAGA  
 1621 -----+-----+-----+-----+-----+-----+ 1680  
 TTGTCCTTAAGGGAGTCGTTCCGAGTGTCTTCGACTTTCACCTCTTCGAAGACTTCAATCT  
 Eco57I  
 MboII  
 MseI |  
 BbsI | | SfaNI  
 MaeII | | | BceFI  
 AflIII | | | | MboII | MaeIII FokI CjeI  
 | | | | | |  
 AGACACGTTAAGAAGAAAAGTCATTGGTCAAAATGATGCCGTTACCAGCATTTGCCGTGC  
 1681 -----+-----+-----+-----+-----+-----+ 1740  
 TCTGTGCAATTCTTCTTTTCAGTAACCAAGTTTTACTACGGCAATGGTCGTAACGGCAGC  
 Sth132I  
 DpnI |  
 AlwI | |  
 BstYI | | |  
 MmeI | | |  
 Sau3AI | | |  
 HaeIV | | | BanII  
 TaqI Hin4I | | | Bsp1286I  
 Hpy178III | CjeI | | | NlaIV |  
 MaeII | | | AlwI | | | | CviJI | |  
 Hpy188IX | | | DpnI | | | | BscGI | | |  
 BccI | | | | Sau3AI | | | | | BslI | | | |  
 | | | | | | | | |  
 CATCCGACGTTCTCGAACAGGGATCAAAGATCCTAACCGACCTACGGGCTCCTTCCTATT  
 1741 -----+-----+-----+-----+-----+-----+ 1800  
 GTAGGCTGCAAGAGCTTGTCCCTAGTTTCTAGGATTGGCTGGATGCCCCAGGAAGGATAA

Figure 19 (Cont.)

```

      MspI
      BsaWI|
      BsrFI|
      PinAI|
      CviJI  ||
      HaeIII  ||
      Sau96I  ||
BsaJI  | | | |
StyI   | | | |   BslI   Cac8I   SfcI
      | | | |   | | | |   | | | |
CCTTGGGCCTACCGGTGTAGGGAAAAGCCTGCTCGCCCAACAAATTGCTATAGAGATGTT
1801 -----+-----+-----+-----+-----+-----+ 1860
      GGAACCCGGATGGCCACATCCCTTTTCGGACGAGCGGTTGTTTAACGATATCTCTACAA

      ApoI
      Tsp509I
      NlaIII
      BbvI  | |
      HgaI  RsaI  | | |
      MboII  TatI  | | | |
      CjePI  Hpy188IX | | | | |
      HinfI  NlaIII  | | | | |
      TfiI  AflIII  | | | | |
      Hpy188IX| PciI  | | | | |
      HphI| | | MjaIV | | | | | Fnu4HI
      BbsI | | | | AccI | | NspI | | | | | TseI |
      | | | | | | | | | | | | | | |
CGGTGGTGAAGACGCTCTGATTCAGGTAGACATGTCAGAGTACATGGAGAAATTTGCTGC
1861 -----+-----+-----+-----+-----+-----+ 1920
      GCCACCACTTCTGCGAGACTAAGTCCATCTGTACAGTCTCATGTACCTCTTTAAACGACG

      DpnI
      CjeI  |
      Sau3AI |
      BccI  | |
      BstXI | | | ScrFI
      HphI  | | | AlwI  |
      BpmI  | | | | EcoRII | MnlI  RcaI  | Sau96I | | BslI
      | | | | | | | | | | | | | | |
TACCÀAGATGATGGGATCACCTCCAGGATATGTAGGTCATGAAGAAGGGGGCCACCTTAC
1921 -----+-----+-----+-----+-----+-----+ 1980
      ATGGTTCTACTACCCTAGTGGAGGTCCTATACATCCAGTACTTCTTCCCCCGGTGGAATG

      MaeII
      Bcefi  RsaI |
      | | |
GGAACAGGTACGTCGCCGTCCTTACTGCGTTGTTCTCTTTGATGAGATAGAAAAGGCACA
1981 -----+-----+-----+-----+-----+-----+ 2040
      CCTTGTCATGCAGCGGCAGGAATGACGCAACAAGAGAACTACTCTATCTTTTCCGTGT

```

87/111

Figure 19 (Cont.)

	TaqII		ApoI		AatII		
	AvaII		Tsp509I		BsaHI		HinfI
	Sau96I		CviRI		MaeII		TfiI
2041	CCCAGACATTATGGACCTGATGTTGCAAATTTTAGAGCAAGGACGTCTTACTGATTCTTT -----+-----+-----+-----+-----+-----+-----+ 2100 GGGTCTGTAATACCTGGACTACAACGTTTAAATCTCGTTCCTGCAGAATGACTAAGAAA						
							DpnI
					Tsp509I		Hin4I
					AceIII		Sau3AI
					NlaIII		AluI
					Hpy178III		CviJI
			NlaIII		RcaI		MnlI
2101	TGGTCGCAAAGTGGATTTCCGTCATGCCATTATTATCATGACCTCCAATTTGGGAGCTGA -----+-----+-----+-----+-----+-----+ 2160 ACCAGCGTTTCACCTAAAGGCAGTACGGTAATAATAGTACTGGAGGTTAAACCCTCGACT						
							BsmFI
			Tsp509I				
		BplI					
		AciI			CviJI		FokI
							NdeI
							DrdI
2161	TCTCATTCGTAAAAGCGGAGAAATTGGTTTGGCTTGAAGTCCCATATGGACTATAAGGT -----+-----+-----+-----+-----+-----+ 2220 AGAGTAAGCATTTTCGCCTCTTTAACCAAAACCGAACTTCAGGGTATACCTGATATTCCA						
							DdeI
							CviJI
							MboII
			NlaIII		MseI		Bst4CI
		TaqI	NspI		BseMII		MseI
2221	CATCCAAGAGAAAATCGAACATGCTATGAAGAAACACTTAAAGCCTGAGTTCATTAACCG -----+-----+-----+-----+-----+-----+ 2280 GTAGGTTCTCTTTTAGCTTGTACGATACTTCTTTGTGAATTCGGACTCAAGTAATTGGC						
							Hpy178III
							FokI
					TaqI		HinfI
					HaeIV	AvaI	MnlI
					Hin4I	SmlI	TfiI
					BsmFI	XhoI	Hin4I
					FokI		
2281	TTTGGATGAAAGTGTGATTTCCGTCCCTCGAGAAAGAATCTCTATCGGAGATCATCCA -----+-----+-----+-----+-----+-----+ 2340 AAACCTACTTTCACACTAAAAGGCAGGGGAGCTCTTTCTTAGAGATAGCTCTAGTAGGT						

88/111

Figure 19 (Cont.)

```

                                Hpy178III
                                TaqI|
                                AvaI||
                                SmlI||
                                XhoI||
                                BsrI|||
                                HinfI|||
                                BsmAI|||
                                DpnI   BspGI|||
                                Sau3AI| PleI   |||
                                |   |   |||
                                TTTAGAGATCAACAACTGGACTCGAGACTGAAAACTACCAAATGGCTTTGAACATCCC
2341 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2400
                                AAATCTCTAGTTGTTTGACCTGAGCTCTGACTTTTTGATGGTTTACCGAACTTGTAGGG

                                BtrI
                                BsiHKAI|
                                Bsp1286I|
                                MaeII|
                                Bcefi  ||
                                AlwNI   MaeIII|   Hpy178III   Bcefi  ||
                                HinfI  |   BfaI  |   BsmI   |   BslI   |   ||
                                |   |   |   |   |   |   |   |   |   |
                                AGACTCTGTGATTTCTTCCTAGTAACGAAGGGGCATTCTCCAGAAATGGGAGCACGTCC
2401 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 2460
                                TCTGAGACACTAAAGGAAGGATCATTGCTTCCCCGTAAGAGGTCTTTACCCCTCGTGCAGG

                                MseI
                                Bcefi  |
                                BanII  ||
                                BsiHKAI  ||
                                Bsp1286I  ||
                                SacI   ||
                                DpnI   AluI  ||
                                BstYI  |   CviJI  ||
                                Sau3AI  |   AciI   ||
                                AlwI   |   MboII  ||
                                MnlI   |   RsaI   ||   BfaI  |MnlI|  ||   HinfI
                                |   |   |   |   |   |   |   |   |
                                TCTACGCCGTGTCATTGAGCAGTACCTTGAAGATCCTCTAGCGGAGCTCTTGCTTAAAGA
2461 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 2520
                                AGATGCGGCACAGTAACTCGTCATGGAACCTTCTAGGAGATCGCCTCGAGAACGAATTTCT

```

89/111

Figure 19 (Cont.)

```

                                Pfl11108I
                                AluI |
                                CviJI |
                                Cac8I | |
                                CjePI | | |
                                Cac8I | | | |
                                Hpy178III AluI | | | | | BsaJI CjePI
                                P1eI | CviJI | | | | | StyI ThaI |
                                | | | | | | | | |
GTCCCTGCCGTCAAGAAGCTCGCAAGCTACGAGCAACCTTGGTTGAAAATCGCGTTGCCTT
2521 -----+-----+-----+-----+-----+-----+ 2580
CAGGACGGCAGTTCTTCGAGCGTTCGATGCTCGTTGGAACCAACTTTTAGCGCAACGGAA

                                BseRI
                                Fnu4HI |
                                AluI | |
                                CviJI | |
                                MnlI TseI | | MnlI
                                EarI | | | | | HinfI |
                                BslI | | | | | CviJI TfiI |
EcoNI | | | BbvI MboII | | | BfaI | BslI | |
| | | | | | | | | | | | | | |
TGAAAGGGAAGAAGAGGAGCAGGAAGCTGCTCTCCCTAGCCCTCACTTGGAATCATAGGA
2581 -----+-----+-----+-----+-----+-----+ 2640
ACTTTCCTTCTTCTCCTCGTCCTTCGACGAGAGGGATCGGGAGTGAACCTTAGTATCCT

                                HgiEII
                                BsaJI |
                                TaqI BspMI | | CjeI ScrFI
                                MaeII | CjeI | StyI | | Tth111III | EcoRII |
                                | | | | | | | | | | |
ACGTCGATAACTCCACTACCAAGGCAGGTATCTCCTTGATAAAACGCTATTGTTTGTCTT
2641 -----+-----+-----+-----+-----+-----+ 2700
TGCAGCTATTGAGGTGATGGTTCCTCCATAGAGGAACTATTTTGGGATAACAAACAGGA

                                AciI
                                Sth132I BpmI
                                MaeIII | BscGI |
                                | | | |
GGAGTTACCGCCTTGACGGGTTGTGAAAATCGCACCTT
2701 -----+-----+-----+-----+-----+ 2738
CCTCAATGGCGGAAC TGCCCAACACTTTTAGCGTGGAA

```

90/111

**Figure 20. Restriction enzyme analysis of the *C. pneumoniae* Thioredoxin gene (SEQ ID NO: 19).**

```

                                CviRI
                                Fnu4HI |
                                AluI |
                                BbvI
                                BbsI |
                                MboII |
HinfI      AluI      NlaIII      DdeI      CviJI |
TfiI      BfaI      CviJI      NlaIII      DdeI      TseI |
|          |          |          |          |
GATTCAGGTTCTAGTGAGCTTATGCTCATGGAAGTTCAAGTCTTCTTAGCTGCAAGAAA
1 -----+-----+-----+-----+-----+ 60
CTAAGTCCAAGATCACTCGAATACGAGTACCTTCAAGTTCAGAAGAATCGACGTTCTTTT

                                Hpy178III
                                Tsp509I BsmFI |
                                Bst4CI |TaqI |TaqI|
                                DpnI
                                Sau3AI |
TAACAGGGACAGTAATTGATTTTTTCGAGAAGGGAACTTATGGTAAAGATCATATCAAG
61 -----+-----+-----+-----+ 120
ATTGTCCCTGTCATTAAAGCTAAAAAGCTCTTCCCTTTGAATACCATTTCTAGTATAGTTC

                                BanII
                                Bsp1286I
                                SfaNI|
PleI      Sth132I      CviRI      CviJI ||
ApoI      HinfI      CviRI      CviJI ||
Tsp509I | HinfI      CviRI      CviJI ||
||      |          |          |
TGAAAATTTTGACTCTTTTATTGCATCGGGGCTCGTTCTCGTTGATTCTTTGCAGAATG
121 -----+-----+-----+-----+ 180
ACTTTTAAACTGAGAAAATAACGTAGCCCCGAGCAAGAGCAACTAAAGAAACGTCTTAC

                                NlaIV
                                CviJI|
                                HaeIII|
                                SfaNI|
                                Hin4I      BbvI      AclI
                                Sau96I ||Hpy188IX | FokI | Fnu4HI |
                                ||      |          |          |
GTGTGGCCCCGTGTCGGATGCTCACTCCTATCTTAGAAAATCTTGCTGCGGAACTTCTCA
181 -----+-----+-----+-----+ 240
CACACCGGGGACAGCCTACGAGTGAGGATAGAATCTTTTAGAACGACGCCTTGAAGGAGT

                                RsaI
                                SunI |
                                MaeII |
                                PstI  ||
                                CviRI | ||
                                Cac8I | ||
                                SfcI  | ||
                                CviJI | ||
                                Cac8I | ||
                                ||      ||
TGTCACTATTGGAAAATCAATATAGATGAGAACAGCCTGCAGAAACGTACGAAGT
241 -----+-----+-----+-----+ 300
ACAGTGATAACCTTTTGTATATCTACTCTTGTCTCGTTCGGACGTCTTGCATGCTTCA

```

Figure 20 (Cont.)

```

                                     AvaI
                                     CviJI|
                                     FokI  ||
                                     Sth132I | ||
AluI                               BccI  | |||Pfl1108I
CviJI    AceIII                   MseI  | |||SimI  |
      |      |      |      |      |      |      |      |
CAGCTCTATTCCCTACGCTTATTCTTTTTAAGGATGGGAACGAGGTGGCTCGGGTCGTAGG
301 -----+-----+-----+-----+-----+-----+-----+ 360
GTCGAGATAAGGATGCGAATAAGAAAAATTCCTACCCTTGCTCCACCGAGCCCAGCATCC

MseI      ApoI                               MseI      CviRI
AflIII|    EcoRI                               BbvI  |    Fnu4HI |
SmlI|      Tsp509I                           Cac8I|    TseI|  |
      ||      |      |      |      |      |      |      |
TCTTAAGGATAAAGAATTCCTAACCAATCTTATCAATAAGCACGCTTAAAAAGACGCTGC
361 -----+-----+-----+-----+-----+-----+-----+ 420
AGAATTCCTATTTCTTAAGGATTGGTTAGAATAGTTATTCGTGCGAATTTTCTGCGACG

MseI
SspI  |      HinfI                               Bst4CI
HgaI|| |Bst4CI TfiI      CviRI  BsrDI  |      AlwI
      ||      |      |      |      |      |      |
AATATTTAAACCGTAGGATTCTTTTGCAATGCTACGGTTTTCTGCCTTACCACTTCATATA
421 -----+-----+-----+-----+-----+-----+-----+ 480
TTATAATTTGGCATCCTAAGAAAACGTTACGATGCCAAAAGACGGAATGGTGAAGTATAT

ApoI
Tsp509I
AluI  |
CviJI |
BsrI  | |
DpnI      TspRI | |
Sau3AI |    BslI  | | |
      | |      | | | |
AAACGATCCCTACACTGGTAGCTAAATTT
481 -----+-----+-----+-----+-----+ 509
TTTGCTAGGGATGTGACCATCGATTAA

```

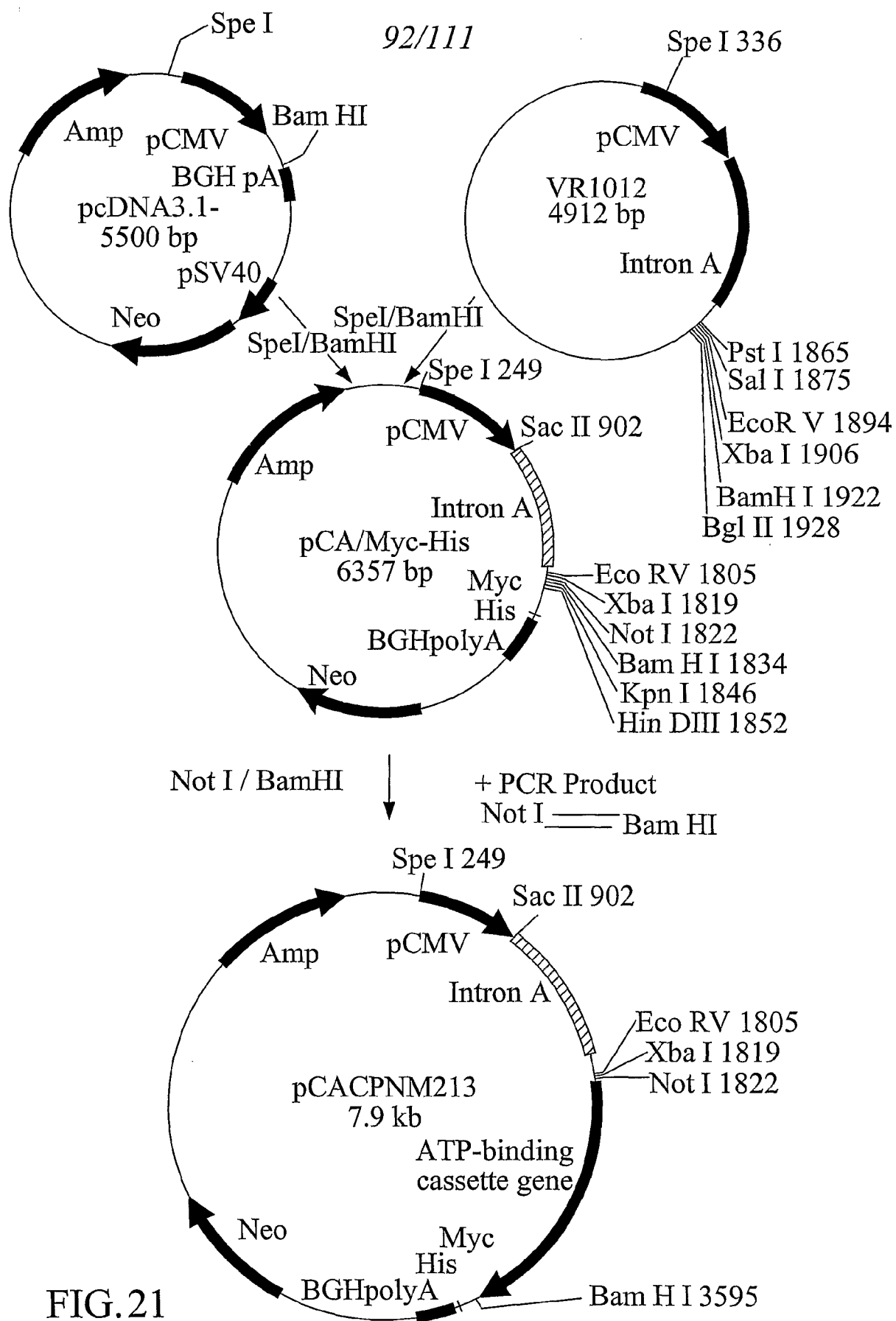
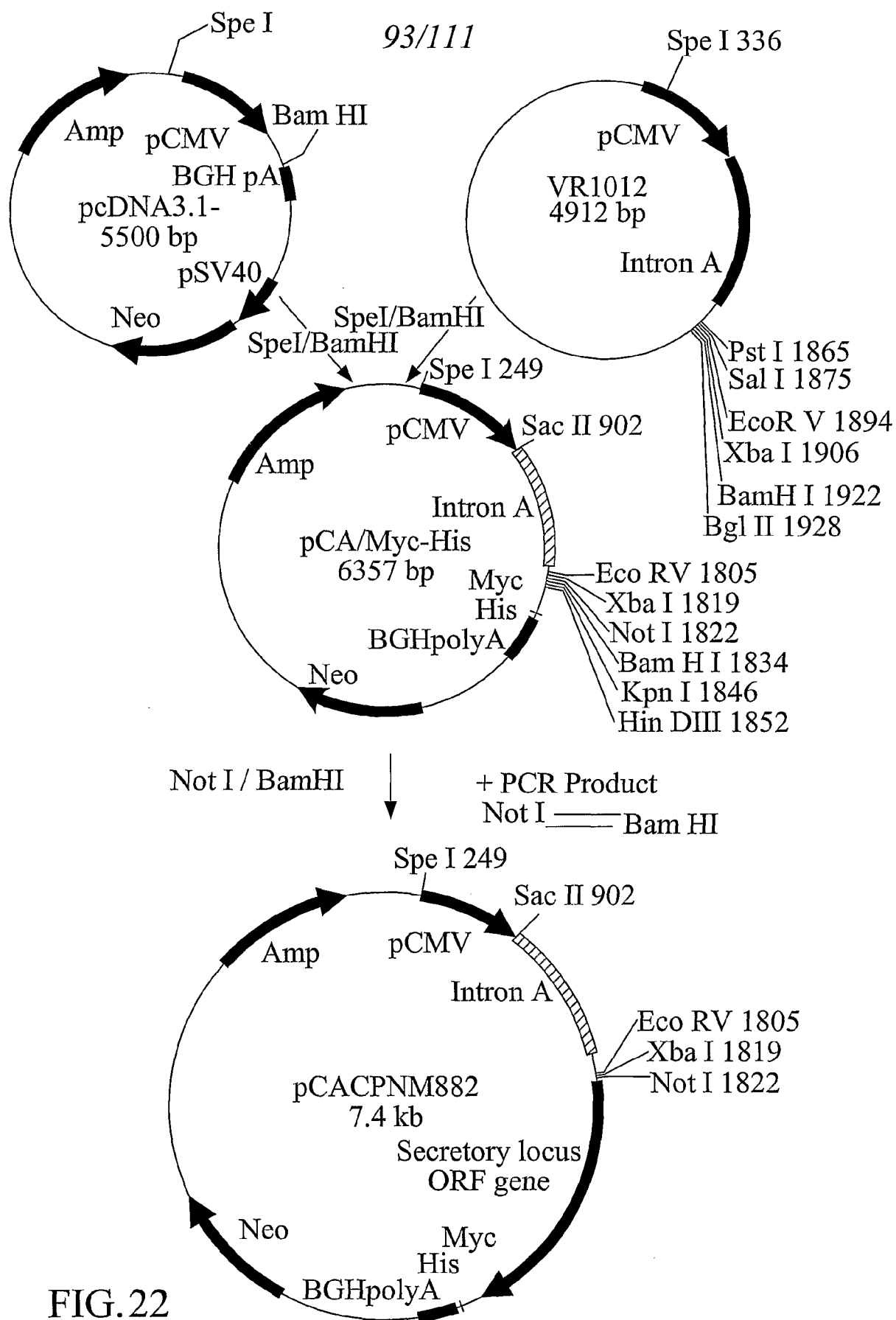
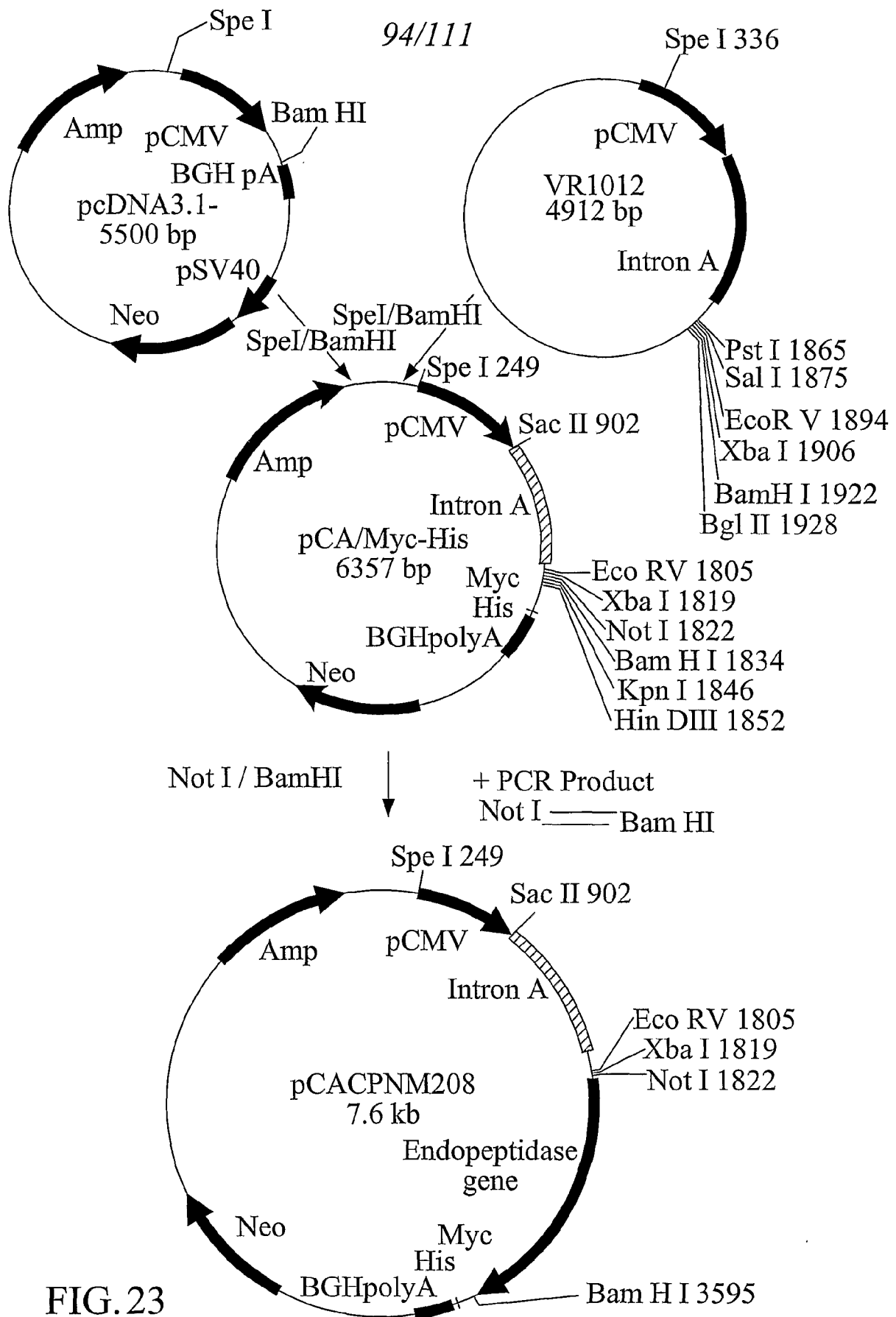


FIG.21  
Construction of pCACPNM213

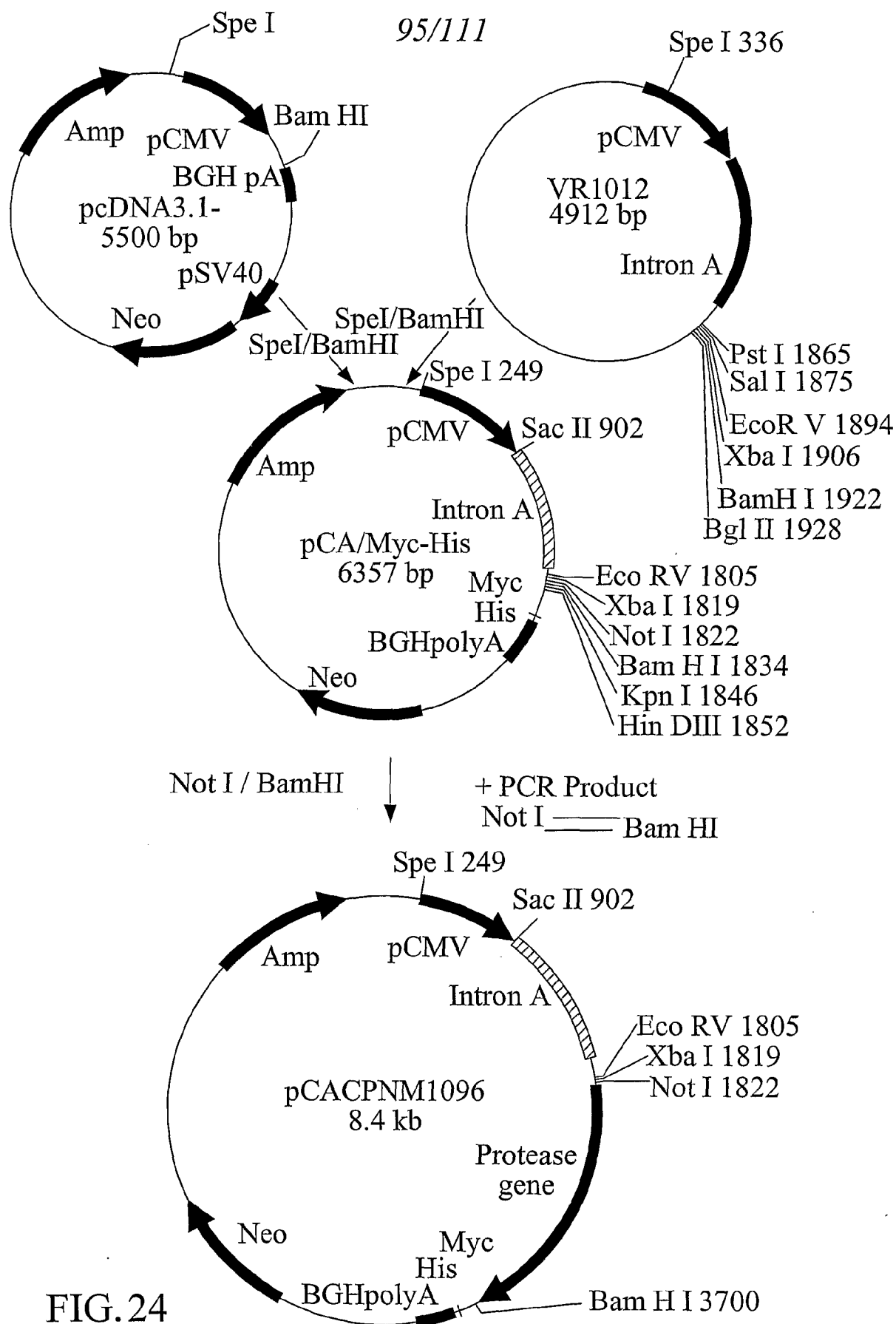




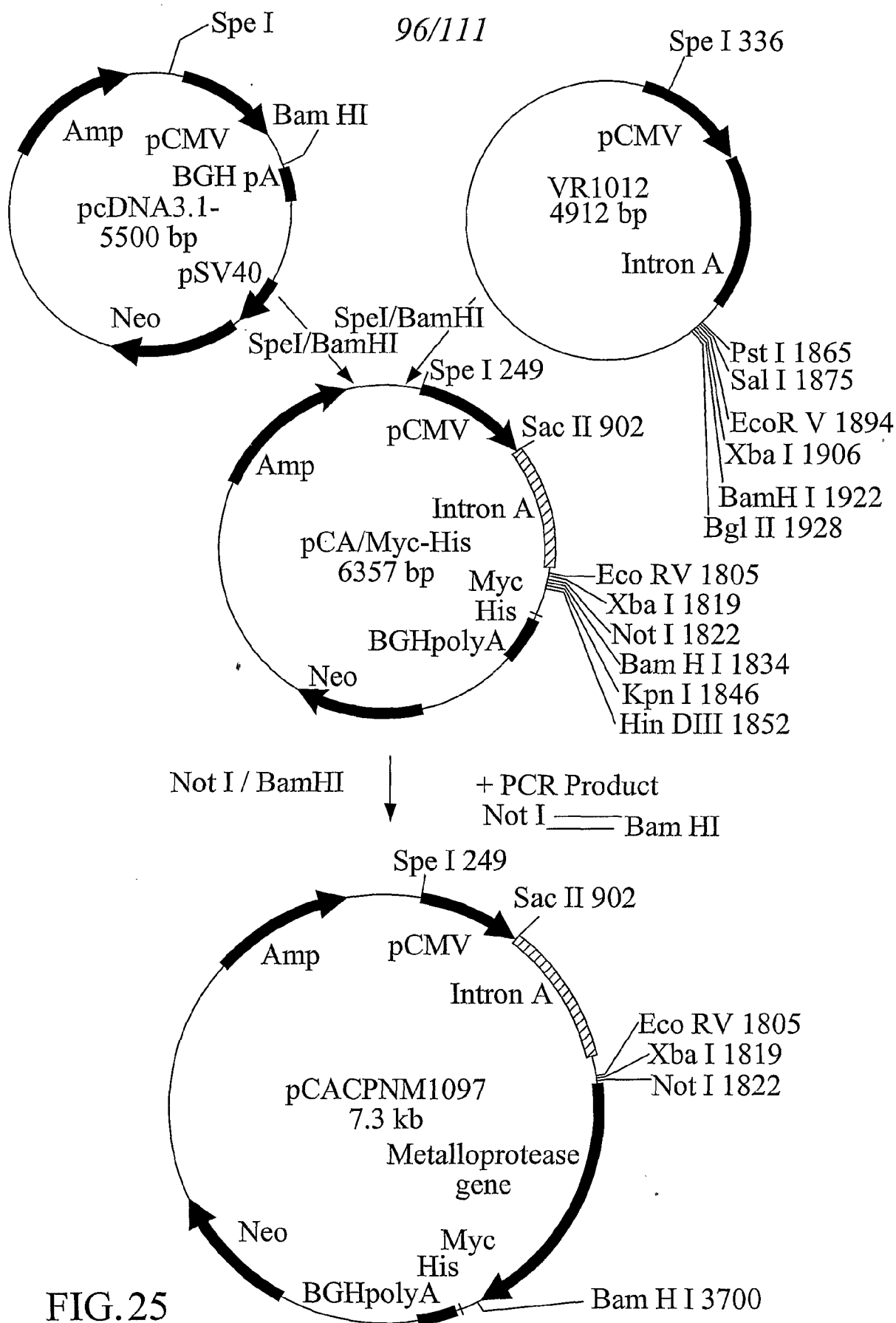
**FIG. 22**  
Construction of pCACPNM882



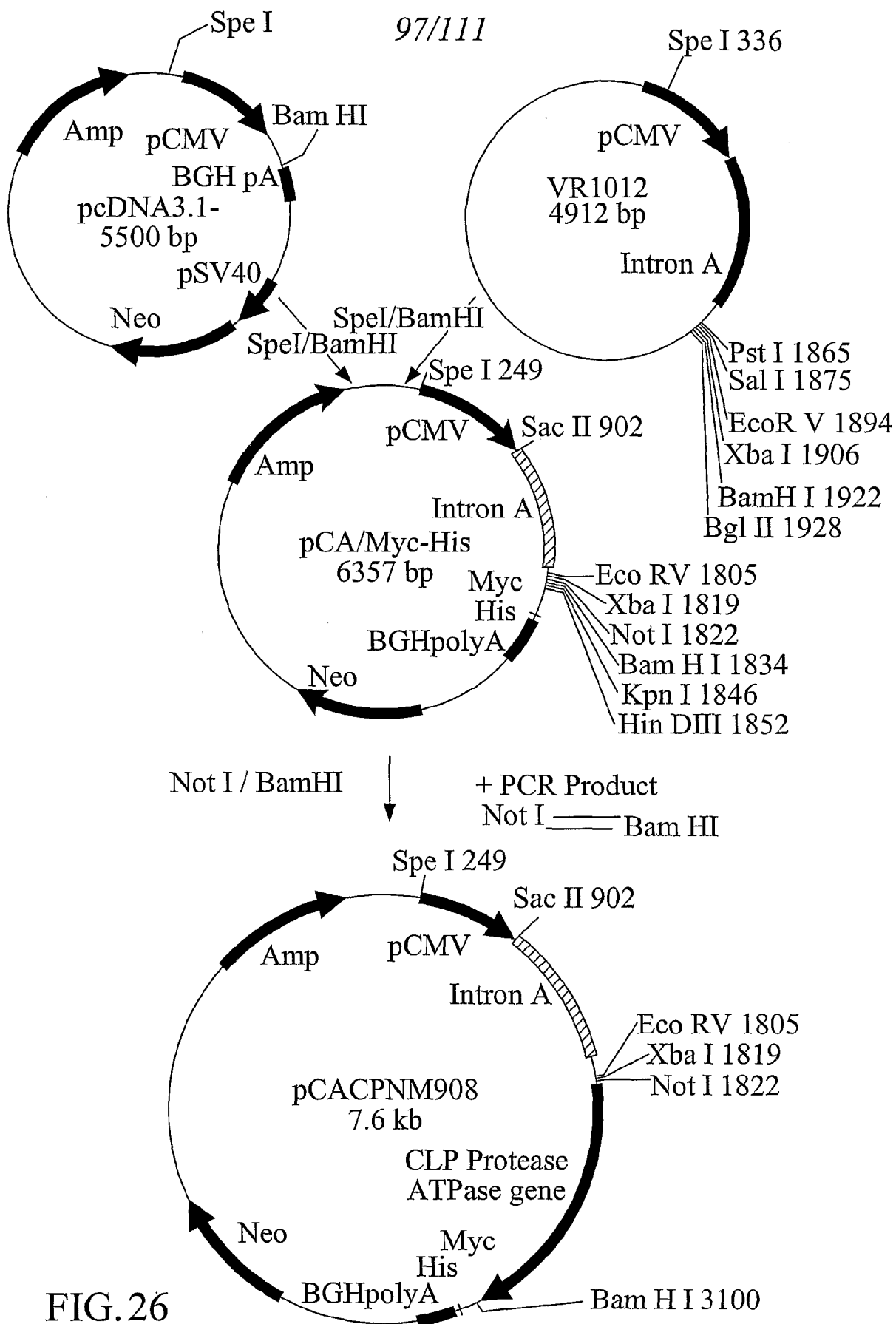
**FIG. 23**  
Construction of pCACP208



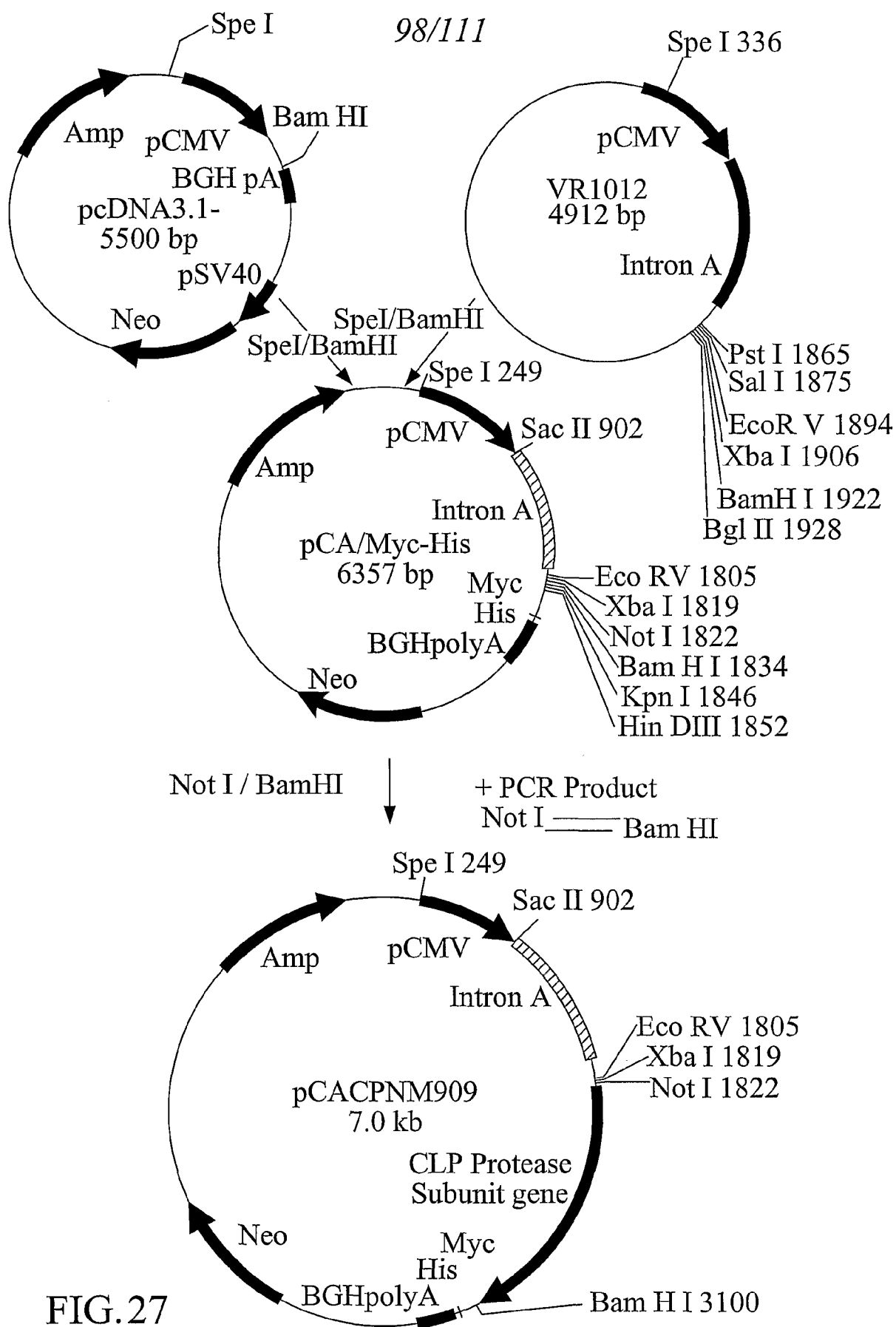
**FIG. 24**  
Construction of pCACPNM1096

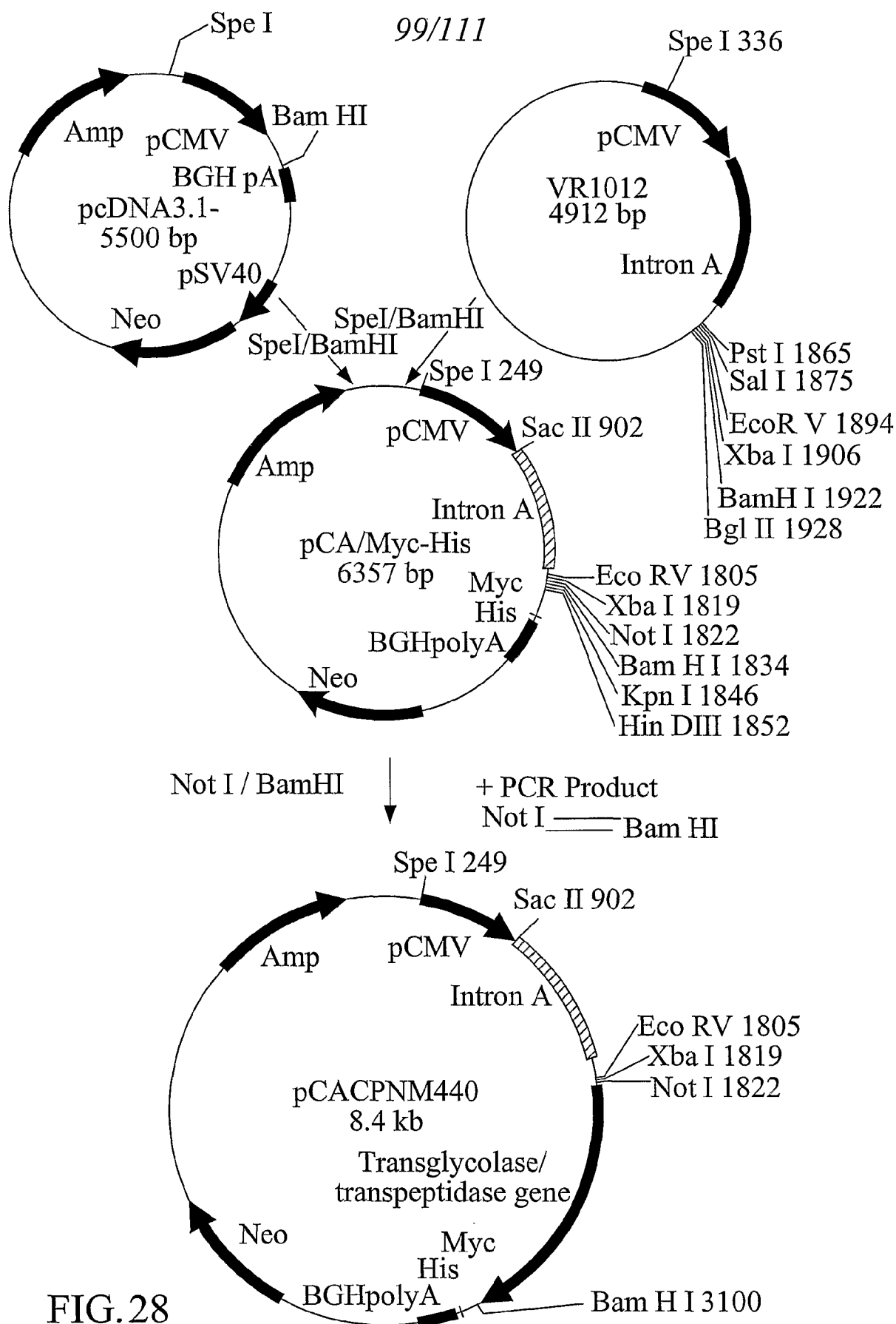


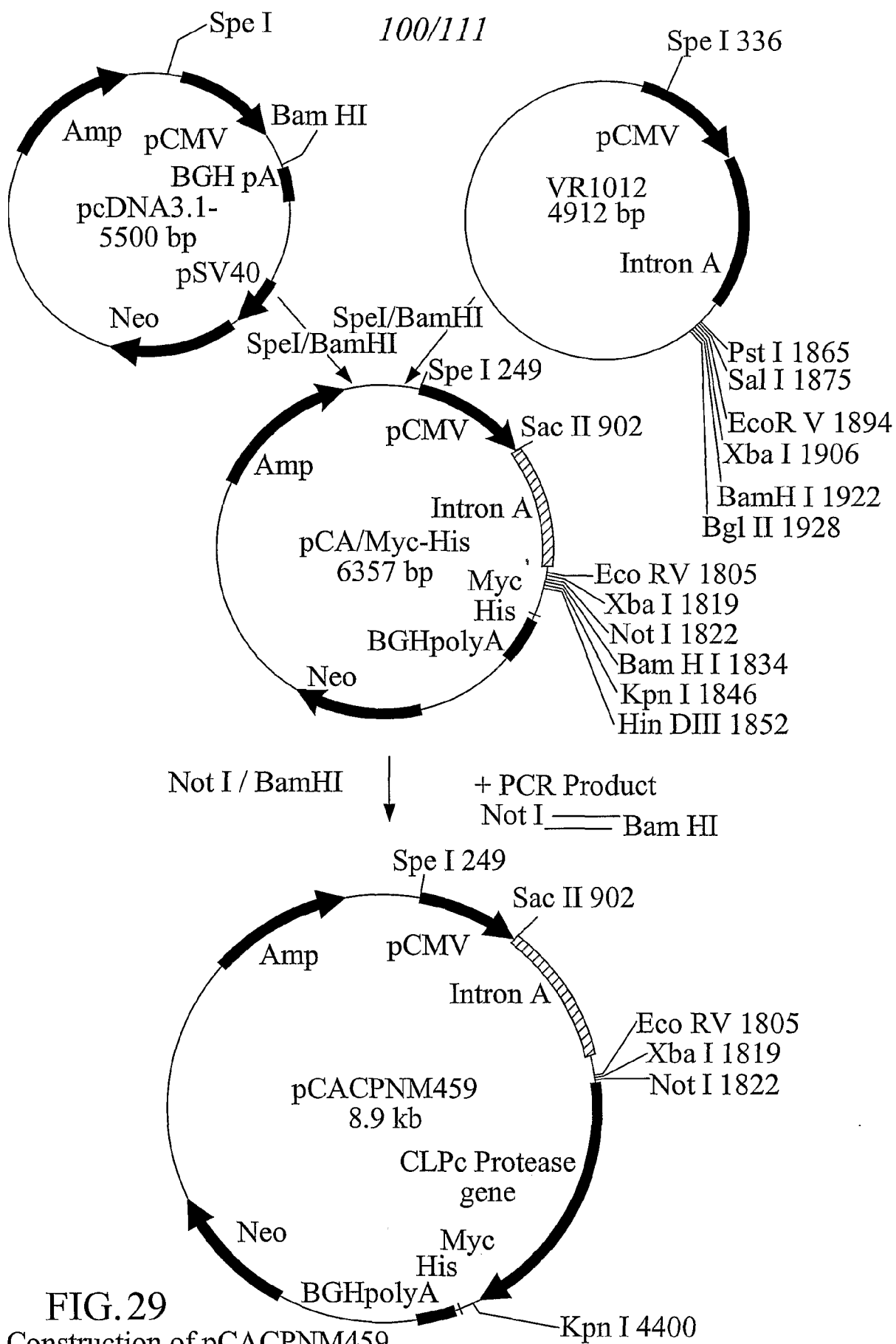
**FIG. 25**  
Construction of pCACPNM1097



**FIG. 26**  
Construction of pCACPNM908

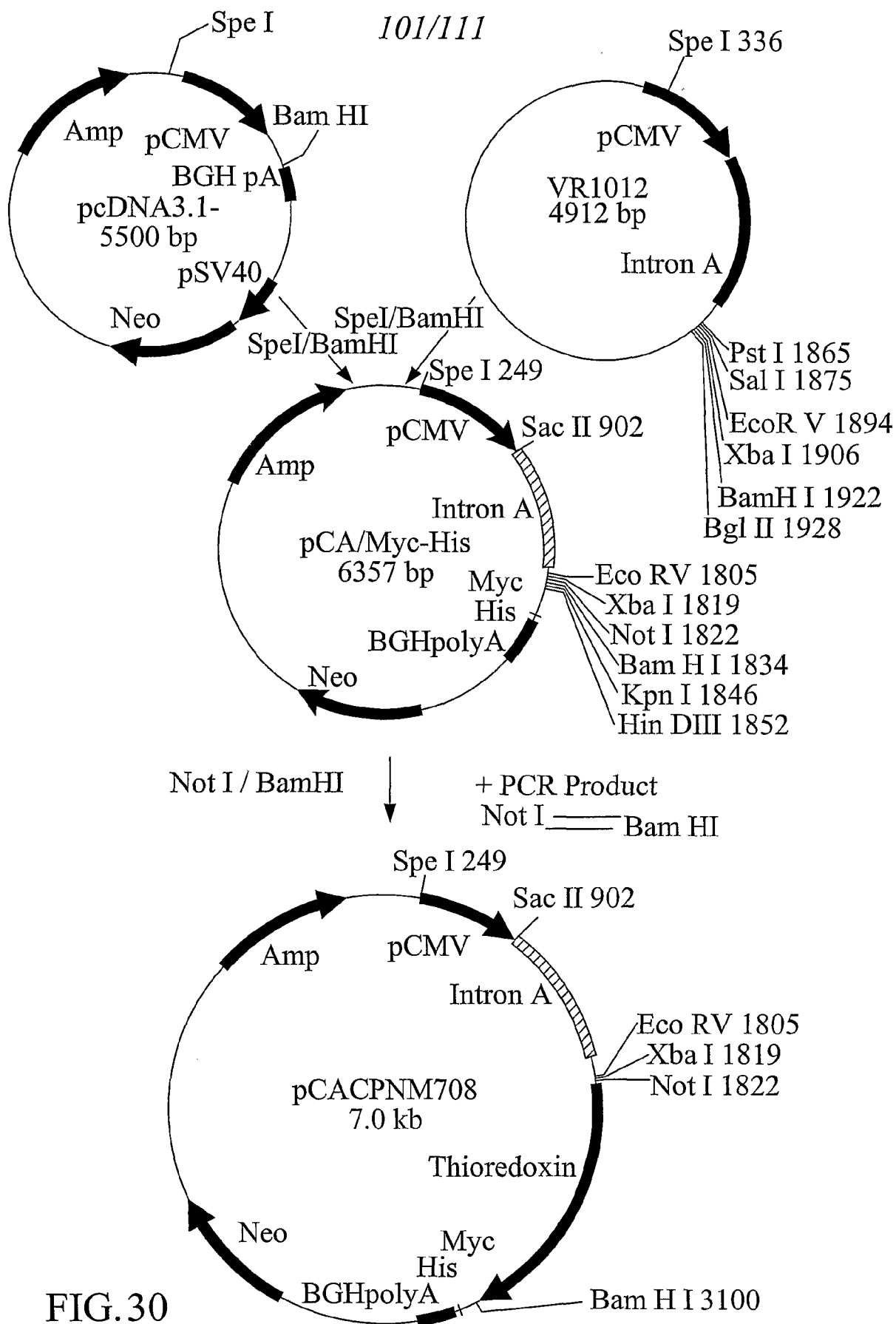






**FIG. 29**  
Construction of pCACPNM459

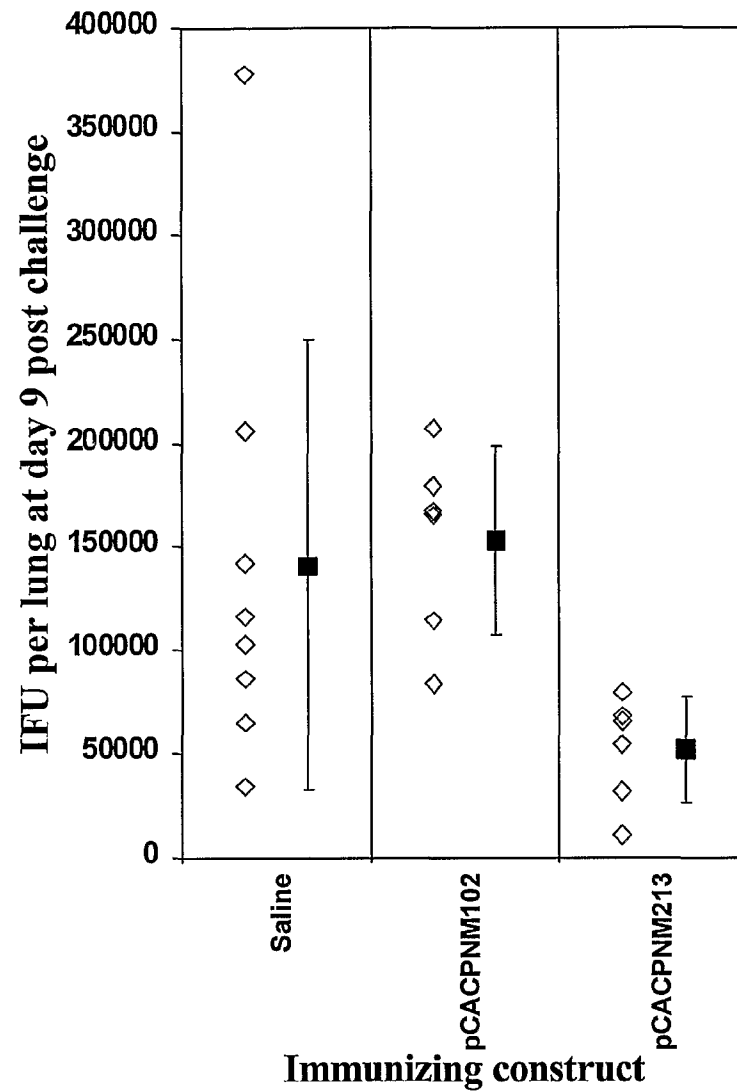




**FIG.30**  
Construction of pCACPNM708

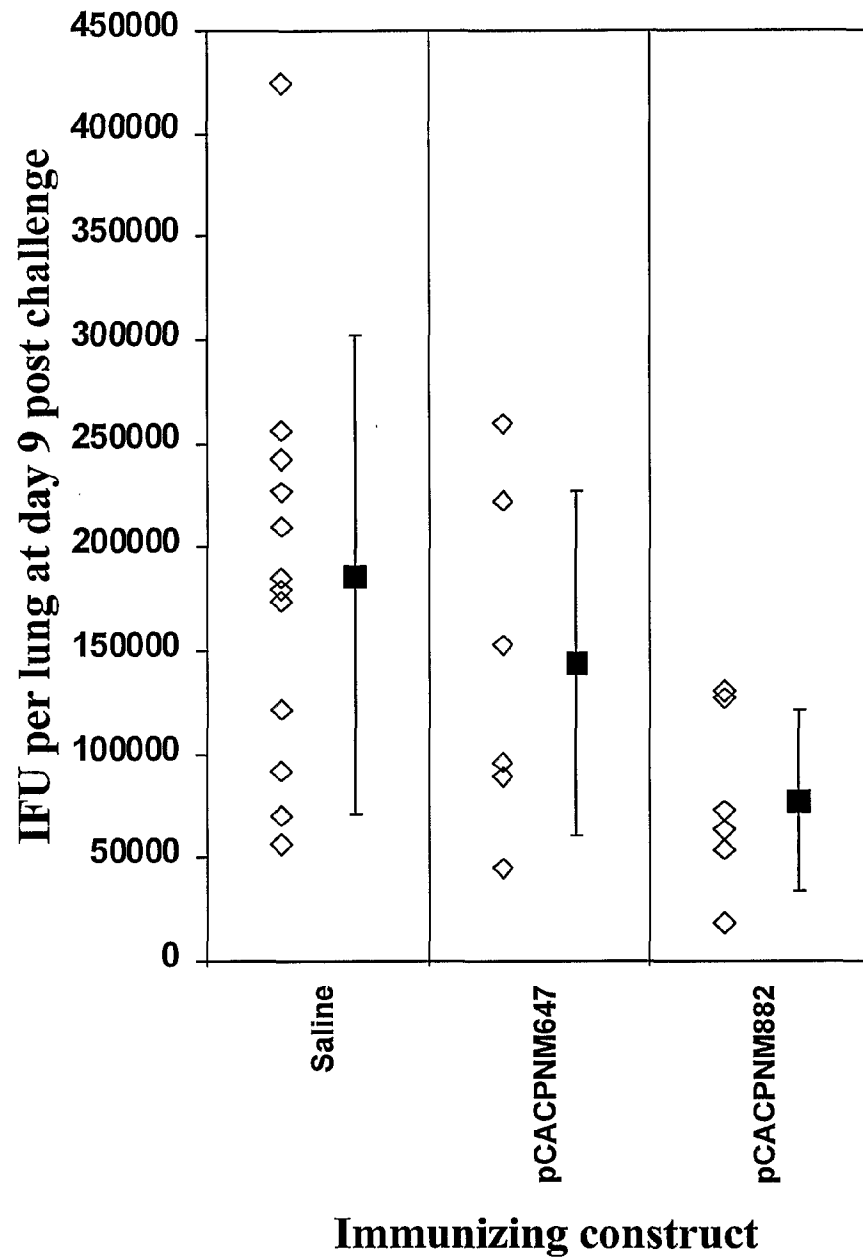
102/111

Figure 31: Protective efficacy of DNA immunization with pCACPNNM213.



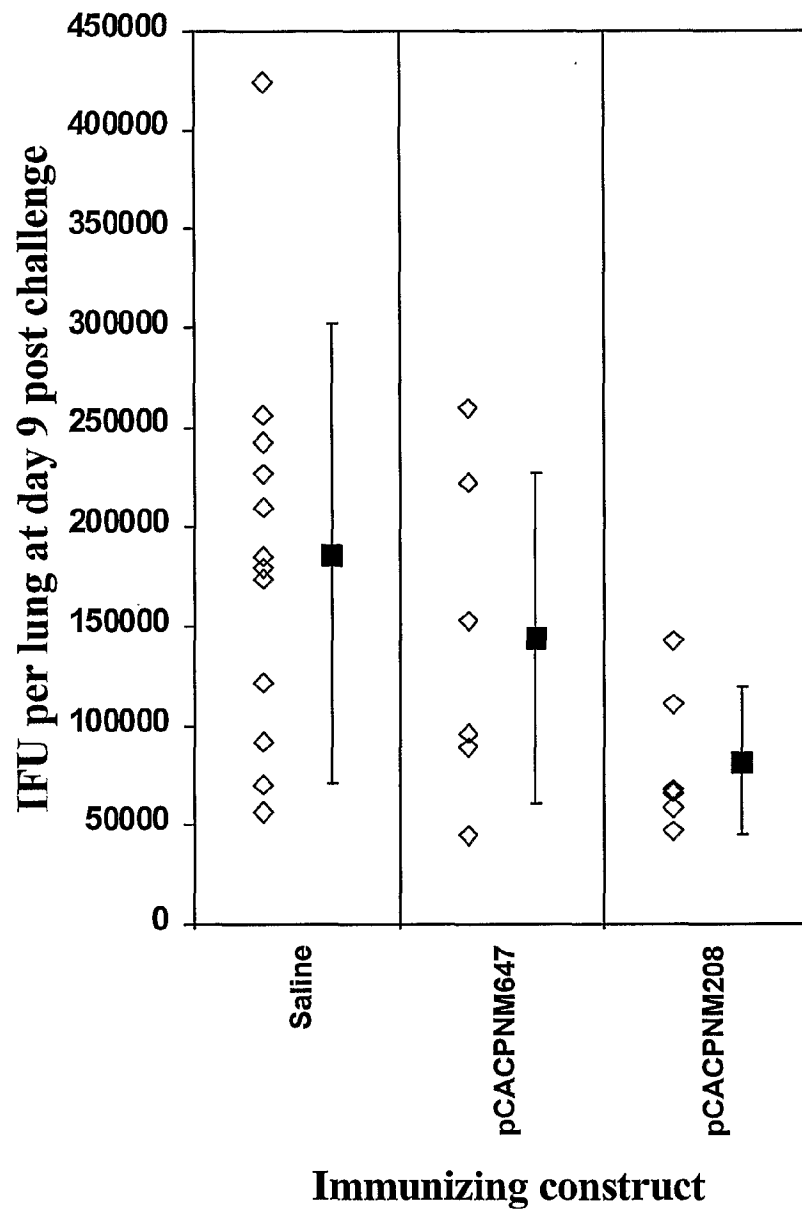
103/111

Figure 32: Protective efficacy of DNA immunisation with pCACPNM882.



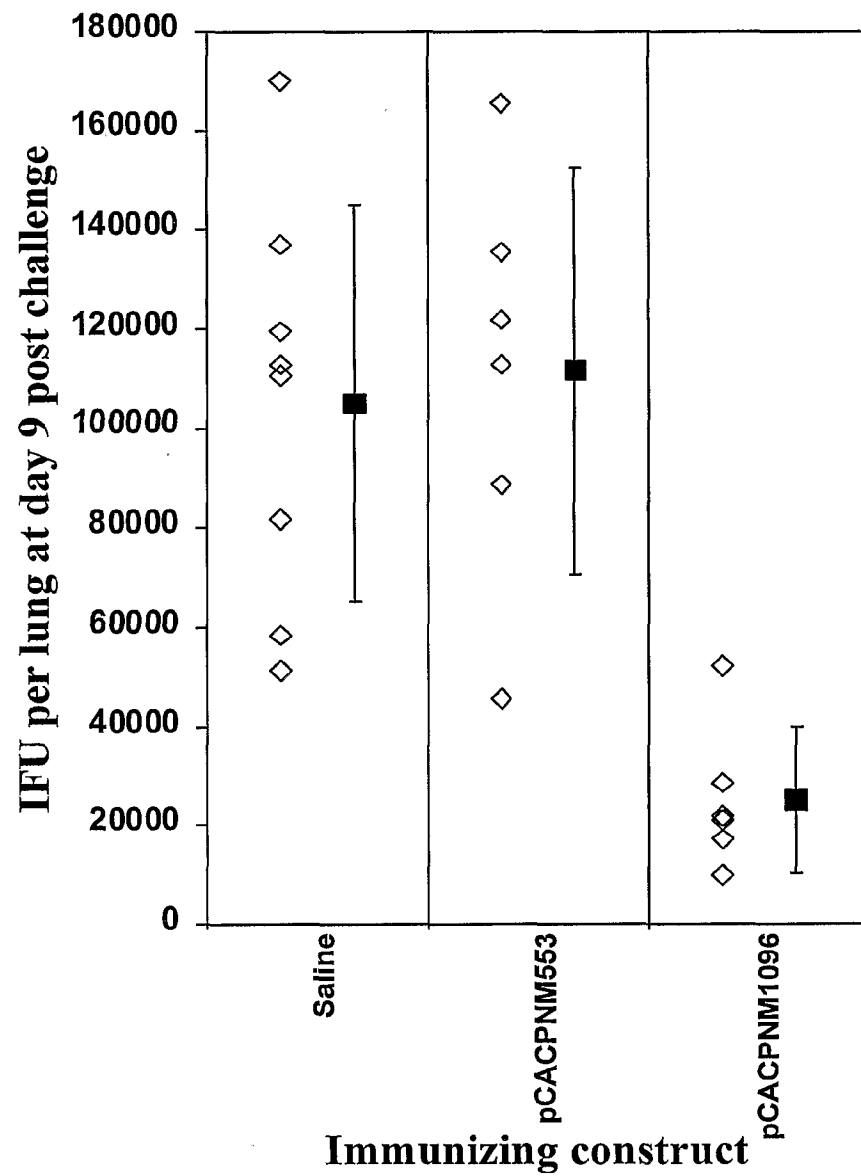
104/111

Figure 33: Protective efficacy of DNA Immunisation with pCACP NM208.



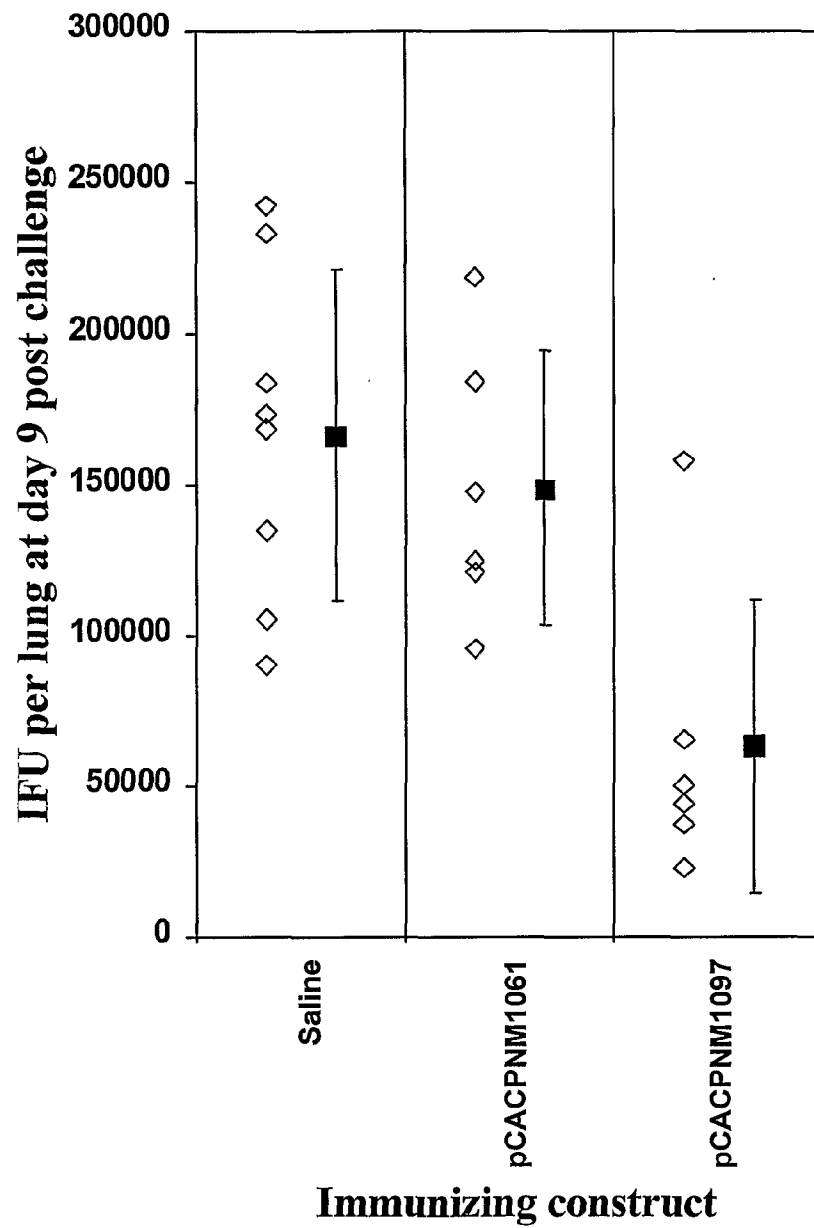
105/111

Figure 34: Protective efficacy of DNA Immunisation with pCACPMM1096.



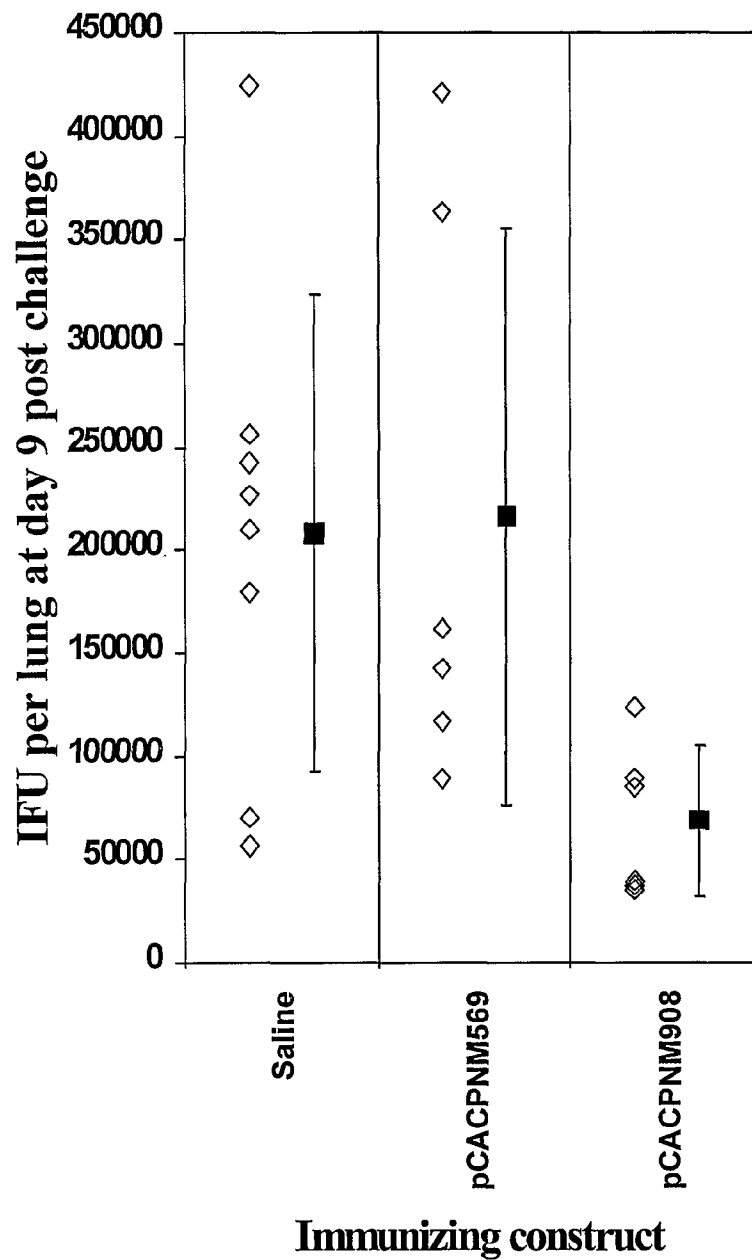
106/111

Figure 35: Protective efficacy of DNA Immunisation with pCACPMM1097.



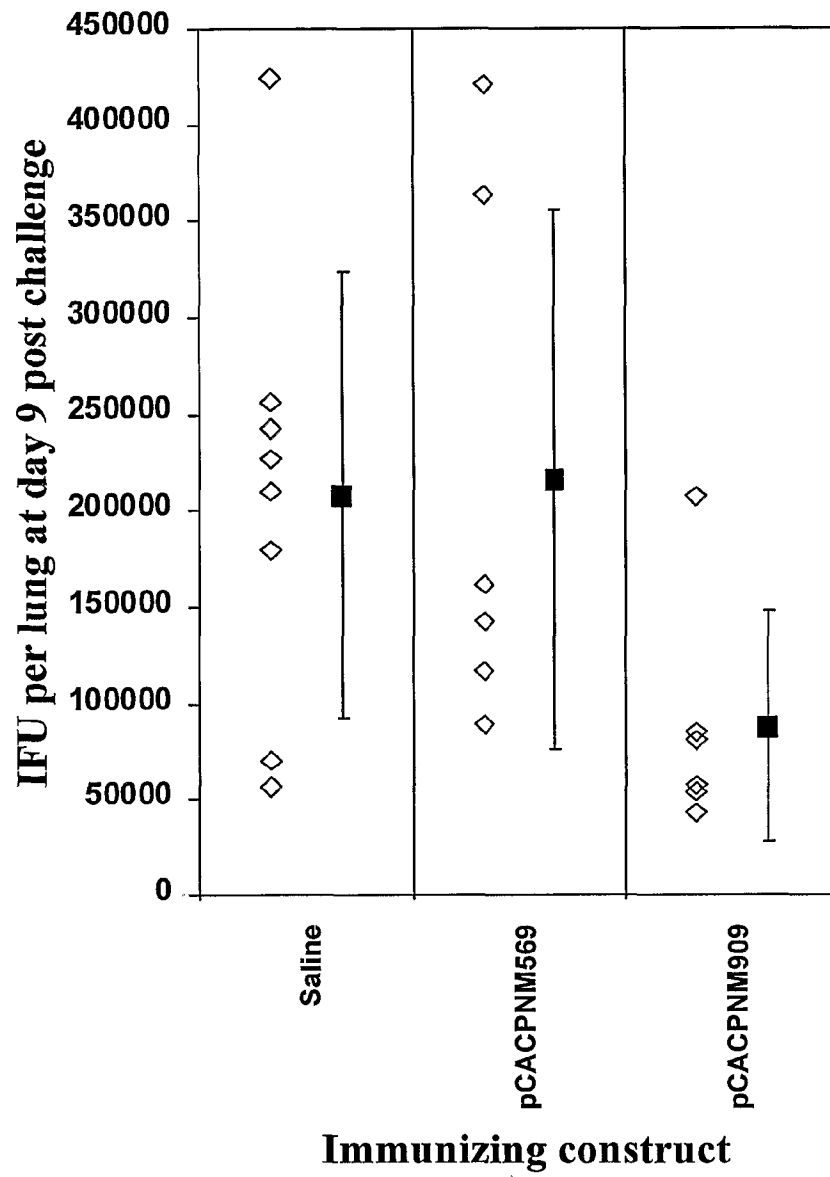
107/111

Figure 36: Protective efficacy of DNA Immunisation with pCACP NM908.



108/111

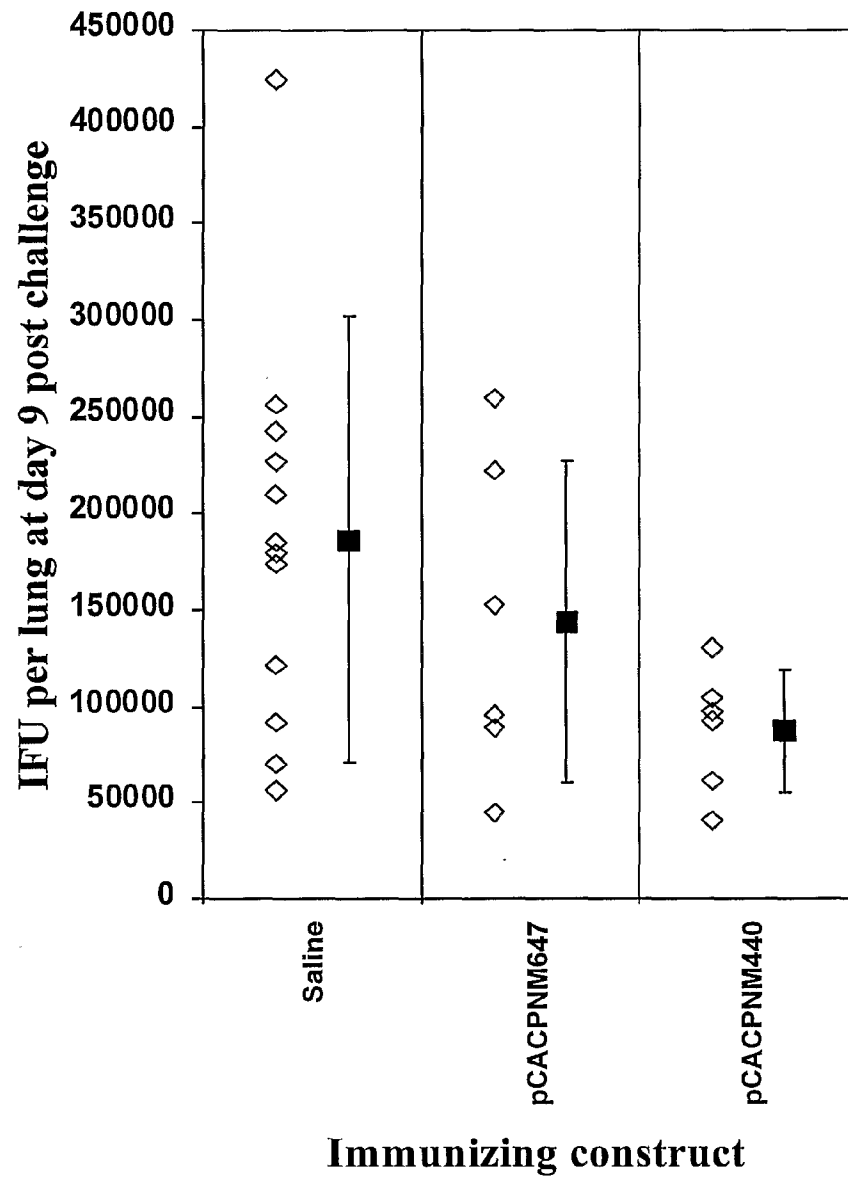
Figure 37: Protective efficacy of DNA Immunisation with pCACPNM909.





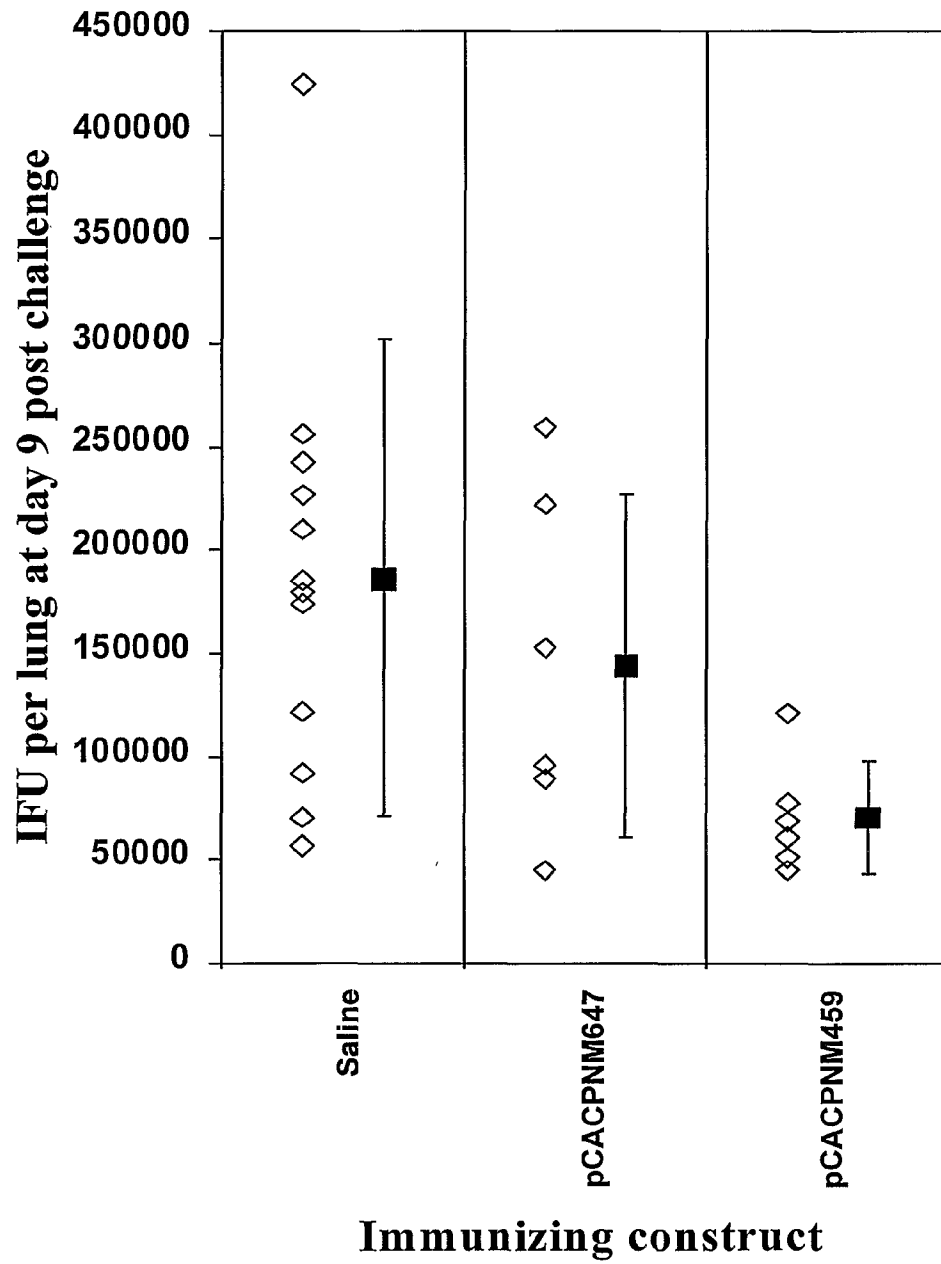
109/111

Figure 38: Protective efficacy of DNA Immunisation with pCACPNM440.



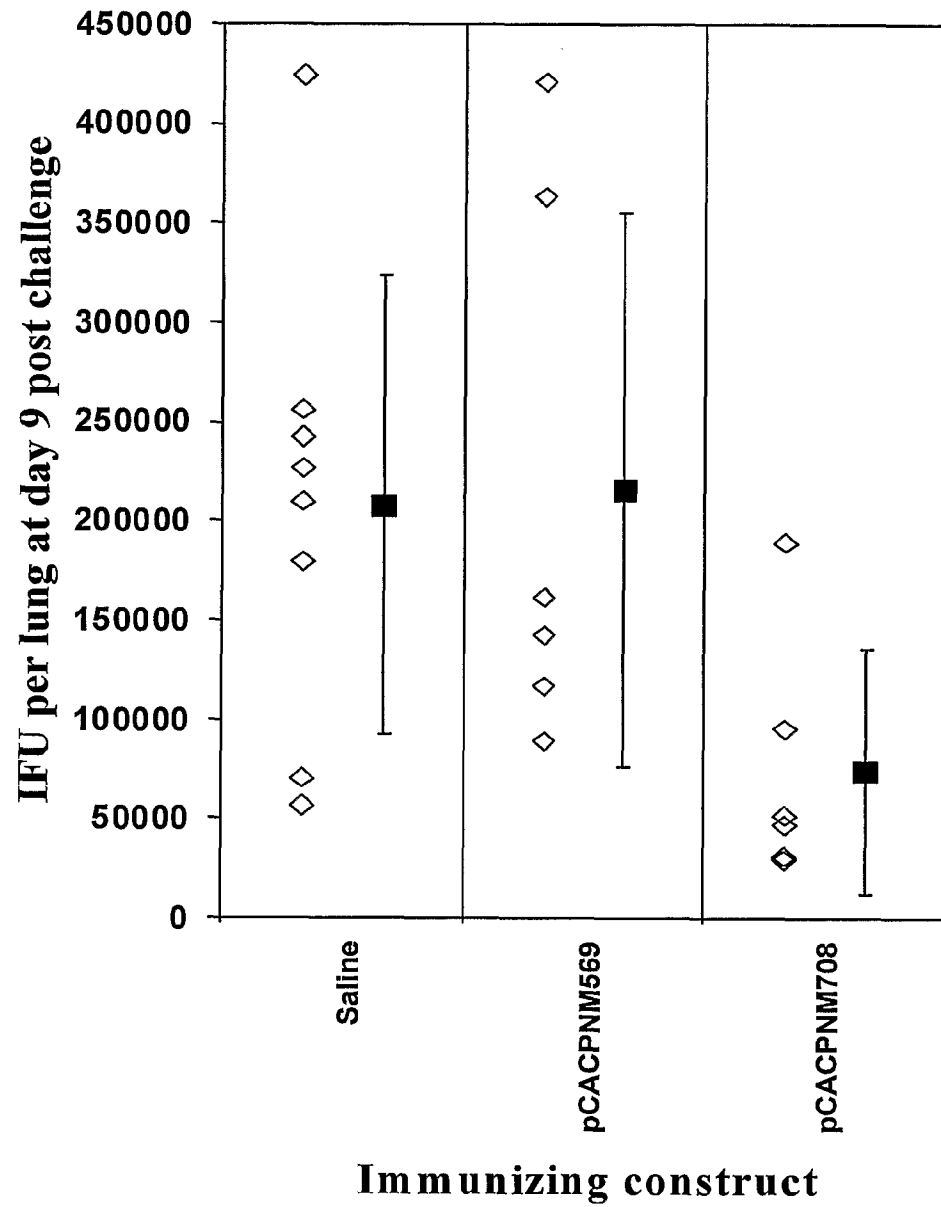
110/111

Figure 39: Protective efficacy of DNA Immunisation with pCACP NM459.



111/111

Figure 40: Protective efficacy of DNA Immunisation with pCACPNM708.



## SEQUENCE LISTING

<110> Aventis Pasteur Limited  
 <120> Chlamydia antigens and corresponding DNA fragments and uses thereof  
 10 <130> 77813-57  
 <140> to be assigned  
 <141>  
 <150> US 60/194,475  
 <151> 2000-04-04  
 <160> 74  
 20 <170> PatentIn Ver. 2.0  
 <210> 1  
 <211> 1787  
 <212> DNA  
 <213> Chlamydia pneumoniae  
 <220>  
 <221> CDS  
 30 <222> (101)..(1684)  
 <400> 1  
 aatctcattc ccccatcgac taaatccacc acggactccg acctcccatg tcttcaatcc 60  
 atatgaacgt aatattaagt agcaaattga gtactatata atg aag atg cat agg 115  
 Met Lys Met His Arg  
 1 5  
 ctt aaa cct acc tta aaa agt ctg atc cct aat ctt ctt ttc tta ttg 163  
 40 Leu Lys Pro Thr Leu Lys Ser Leu Ile Pro Asn Leu Leu Phe Leu Leu  
 10 15 20  
 ctc act ctt tca agc tgc tca aag caa aaa caa gaa ccc tta gga aaa 211  
 Leu Thr Leu Ser Ser Cys Ser Lys Gln Lys Gln Glu Pro Leu Gly Lys  
 25 30 35  
 cat ctc gtt att gcg atg agc cat gat ctc gcc gac cta gat cct cgc 259  
 His Leu Val Ile Ala Met Ser His Asp Leu Ala Asp Leu Asp Pro Arg  
 40 45 50  
 50 aat gcc tat tta agc aga gat gct tcc cta gca aaa gcc ctc tat gaa 307  
 Asn Ala Tyr Leu Ser Arg Asp Ala Ser Leu Ala Lys Ala Leu Tyr Glu  
 55 60 65  
 gga ctg aca aga gaa act gat caa gga atc gca ctg gct ctt gca gaa 355  
 Gly Leu Thr Arg Glu Thr Asp Gln Gly Ile Ala Leu Ala Leu Ala Glu  
 70 75 80 85  
 agt tat acc ctg tca aaa gat cat aag gtc tat acc ttt aaa ctc aga 403  
 60 Ser Tyr Thr Leu Ser Lys Asp His Lys Val Tyr Thr Phe Lys Leu Arg  
 90 95 100

	cct tct gtg tgg agc gat ggc act cca ctc act gct tat gac ttt gaa	451
	Pro Ser Val Trp Ser Asp Gly Thr Pro Leu Thr Ala Tyr Asp Phe Glu	
	105 110 115	
	aaa tct ata aaa caa ctg tac ttc gaa gaa ttt tca cct tcc ata cat	499
	Lys Ser Ile Lys Gln Leu Tyr Phe Glu Glu Phe Ser Pro Ser Ile His	
	120 125 130	
10	act tta ctc ggc gtg att aaa aat tct tcg gca atc cac aat gct caa	547
	Thr Leu Leu Gly Val Ile Lys Asn Ser Ser Ala Ile His Asn Ala Gln	
	135 140 145	
	aaa tct ctg gaa act ctt ggg ata cag gca aaa gat gat ctt act ttg	595
	Lys Ser Leu Glu Thr Leu Gly Ile Gln Ala Lys Asp Asp Leu Thr Leu	
	150 155 160 165	
20	gtg att acc cta gag caa cct ttc cca tac ttt ctc aca ctt atc gct	643
	Val Ile Thr Leu Glu Gln Pro Phe Pro Tyr Phe Leu Thr Leu Ile Ala	
	170 175 180	
	cgc ccc gta ttc tcc cct gtt cat cac acc ctt agg gaa tcc tat aag	691
	Arg Pro Val Phe Ser Pro Val His His Thr Leu Arg Glu Ser Tyr Lys	
	185 190 195	
	aaa gga aca ccc cca tcc aca tac atc tcc aat ggg ccc ttt gtc tta	739
	Lys Gly Thr Pro Pro Ser Thr Tyr Ile Ser Asn Gly Pro Phe Val Leu	
	200 205 210	
30	aaa aaa cat gaa cac caa aac tac tta att tta gaa aaa aat cct cac	787
	Lys Lys His Glu His Gln Asn Tyr Leu Ile Leu Glu Lys Asn Pro His	
	215 220 225	
	tac tat gat cat gaa tca gta aag tta gac cga gtc acc tta aaa att	835
	Tyr Tyr Asp His Glu Ser Val Lys Leu Asp Arg Val Thr Leu Lys Ile	
	230 235 240 245	
40	atc cca gac gcc tcc aca gcc acg aaa ctt ttc aaa agt aaa tct ata	883
	Ile Pro Asp Ala Ser Thr Ala Thr Lys Leu Phe Lys Ser Lys Ser Ile	
	250 255 260	
	gat tgg att ggc tca cct tgg agc gct ccg ata tct aac gaa gac caa	931
	Asp Trp Ile Gly Ser Pro Trp Ser Ala Pro Ile Ser Asn Glu Asp Gln	
	265 270 275	
	aaa gtt ctc tcc caa gaa aag att ctt acc tat tct gtt tca agc acc	979
	Lys Val Leu Ser Gln Glu Lys Ile Leu Thr Tyr Ser Val Ser Ser Thr	
	280 285 290	
50	acc ctt ctt atc tat aac ctg caa aaa cct cta ata caa aat aaa gcc	1027
	Thr Leu Leu Ile Tyr Asn Leu Gln Lys Pro Leu Ile Gln Asn Lys Ala	
	295 300 305	
	ctc agg aaa gcc att gct cat gct att gat aga aaa tct atc tta aga	1075
	Leu Arg Lys Ala Ile Ala His Ala Ile Asp Arg Lys Ser Ile Leu Arg	
	310 315 320 325	
60	ctc gtg cct tca gga caa gaa gct gta act cta gtt ccc cca aat ctt	1123
	Leu Val Pro Ser Gly Gln Glu Ala Val Thr Leu Val Pro Pro Asn Leu	
	330 335 340	

tca caa ctc aat ctt caa aaa gag atc tca aca gaa gaa cga caa aca 1171  
 Ser Gln Leu Asn Leu Gln Lys Glu Ile Ser Thr Glu Glu Arg Gln Thr  
 345 350 355  
 aaa gcc aga gca tat ttt caa gaa gct aaa gaa aca ctt tct gaa aaa 1219  
 Lys Ala Arg Ala Tyr Phe Gln Glu Ala Lys Glu Thr Leu Ser Glu Lys  
 360 365 370  
 10 gaa ctc gca gaa ctc agc atc ctc tat cct ata gat tcc tcg aat tcc 1267  
 Glu Leu Ala Glu Leu Ser Ile Leu Tyr Pro Ile Asp Ser Ser Asn Ser  
 375 380 385  
 tcc atc ata gct caa gaa atc caa aga caa ctt aaa gat acc tta gga 1315  
 Ser Ile Ile Ala Gln Glu Ile Gln Arg Gln Leu Lys Asp Thr Leu Gly  
 390 395 400 405  
 20 ttg aaa atc aaa atc caa ggc atg gag tac cac tgc ttt tta aag aaa 1363  
 Leu Lys Ile Lys Ile Gln Gly Met Glu Tyr His Cys Phe Leu Lys Lys  
 410 415 420  
 cgt cgt caa gga gat ttc ttc ata gcg aca gga gga tgg att gcg gaa 1411  
 Arg Arg Gln Gly Asp Phe Phe Ile Ala Thr Gly Gly Trp Ile Ala Glu  
 425 430 435  
 tac gta agc ccc gta gcc ttc cta tct att cta ggc aac ccc aga gac 1459  
 Tyr Val Ser Pro Val Ala Phe Leu Ser Ile Leu Gly Asn Pro Arg Asp  
 440 445 450  
 30 ctc aca caa tgg aga aac agt gat tac gaa aag act tta gag aaa ctc 1507  
 Leu Thr Gln Trp Arg Asn Ser Asp Tyr Glu Lys Thr Leu Glu Lys Leu  
 455 460 465  
 tat ctc cct cat gcc tac aaa gag aat tta aaa cgc gca gaa atg ata 1555  
 Tyr Leu Pro His Ala Tyr Lys Glu Asn Leu Lys Arg Ala Glu Met Ile  
 470 475 480 485  
 40 ata gaa gaa gaa acc ccg att atc ccc ctg tat cac ggc aaa tat att 1603  
 Ile Glu Glu Glu Thr Pro Ile Ile Pro Leu Tyr His Gly Lys Tyr Ile  
 490 495 500  
 tac gct ata cat cct aaa atc cag aat aca ttc gga tct ctt cta ggc 1651  
 Tyr Ala Ile His Pro Lys Ile Gln Asn Thr Phe Gly Ser Leu Leu Gly  
 505 510 515  
 cac aca gat ctc aaa aat atc gat atc tta agt tagatccgaa atggaaaaat 1704  
 His Thr Asp Leu Lys Asn Ile Asp Ile Leu Ser  
 520 525  
 50 taaaaatttt atagacaatc ttgaaaagag aattaaat ttttaattta aattatagtt 1764  
 gcaattgaaa acgcccctaa gaa 1787

&lt;210&gt; 2

&lt;211&gt; 528

&lt;212&gt; PRT

&lt;213&gt; Chlamydia pneumoniae

60 &lt;220&gt;

&lt;221&gt; SITE

<222> (188)...(61)  
 <223> B-cell epitope  
  
 <220>  
 <221> SITE  
 <222> (345)...(355)  
 <223> B-cell epitope  
  
 10 <220>  
 <221> SITE  
 <222> (434)...(442)  
 <223> T-cell epitope  
  
 <400> 2  
 Met Lys Met His Arg Leu Lys Pro Thr Leu Lys Ser Leu Ile Pro Asn  
     1                    5                    10                    15  
  
 20 Leu Leu Phe Leu Leu Leu Thr Leu Ser Ser Cys Ser Lys Gln Lys Gln  
                     20                    25                    30  
  
 Glu Pro Leu Gly Lys His Leu Val Ile Ala Met Ser His Asp Leu Ala  
             35                    40                    45  
  
 Asp Leu Asp Pro Arg Asn Ala Tyr Leu Ser Arg Asp Ala Ser Leu Ala  
             50                    55                    60  
  
 30 Lys Ala Leu Tyr Glu Gly Leu Thr Arg Glu Thr Asp Gln Gly Ile Ala  
         65                    70                    75                    80  
  
 Leu Ala Leu Ala Glu Ser Tyr Thr Leu Ser Lys Asp His Lys Val Tyr  
                     85                    90                    95  
  
 Thr Phe Lys Leu Arg Pro Ser Val Trp Ser Asp Gly Thr Pro Leu Thr  
             100                    105                    110  
  
 Ala Tyr Asp Phe Glu Lys Ser Ile Lys Gln Leu Tyr Phe Glu Glu Phe  
             115                    120                    125  
  
 40 Ser Pro Ser Ile His Thr Leu Leu Gly Val Ile Lys Asn Ser Ser Ala  
             130                    135                    140  
  
 Ile His Asn Ala Gln Lys Ser Leu Glu Thr Leu Gly Ile Gln Ala Lys  
     145                    150                    155                    160  
  
 Asp Asp Leu Thr Leu Val Ile Thr Leu Glu Gln Pro Phe Pro Tyr Phe  
             165                    170                    175  
  
 50 Leu Thr Leu Ile Ala Arg Pro Val Phe Ser Pro Val His His Thr Leu  
             180                    185                    190  
  
 Arg Glu Ser Tyr Lys Lys Gly Thr Pro Pro Ser Thr Tyr Ile Ser Asn  
             195                    200                    205  
  
 Gly Pro Phe Val Leu Lys Lys His Glu His Gln Asn Tyr Leu Ile Leu  
         210                    215                    220  
  
 60 Glu Lys Asn Pro His Tyr Tyr Asp His Glu Ser Val Lys Leu Asp Arg  
         225                    230                    235                    240

Val Thr Leu Lys Ile Ile Pro Asp Ala Ser Thr Ala Thr Lys Leu Phe  
 245 250 255  
 Lys Ser Lys Ser Ile Asp Trp Ile Gly Ser Pro Trp Ser Ala Pro Ile  
 260 265 270  
 10 Ser Asn Glu Asp Gln Lys Val Leu Ser Gln Glu Lys Ile Leu Thr Tyr  
 275 280 285  
 Ser Val Ser Ser Thr Thr Leu Leu Ile Tyr Asn Leu Gln Lys Pro Leu  
 290 295 300  
 Ile Gln Asn Lys Ala Leu Arg Lys Ala Ile Ala His Ala Ile Asp Arg  
 305 310 315 320  
 Lys Ser Ile Leu Arg Leu Val Pro Ser Gly Gln Glu Ala Val Thr Leu  
 325 330 335  
 20 Val Pro Pro Asn Leu Ser Gln Leu Asn Leu Gln Lys Glu Ile Ser Thr  
 340 345 350  
 Glu Glu Arg Gln Thr Lys Ala Arg Ala Tyr Phe Gln Glu Ala Lys Glu  
 355 360 365  
 Thr Leu Ser Glu Lys Glu Leu Ala Glu Leu Ser Ile Leu Tyr Pro Ile  
 370 375 380  
 30 Asp Ser Ser Asn Ser Ser Ile Ile Ala Gln Glu Ile Gln Arg Gln Leu  
 385 390 395 400  
 Lys Asp Thr Leu Gly Leu Lys Ile Lys Ile Gln Gly Met Glu Tyr His  
 405 410 415  
 Cys Phe Leu Lys Lys Arg Arg Gln Gly Asp Phe Phe Ile Ala Thr Gly  
 420 425 430  
 Gly Trp Ile Ala Glu Tyr Val Ser Pro Val Ala Phe Leu Ser Ile Leu  
 435 440 445  
 40 Gly Asn Pro Arg Asp Leu Thr Gln Trp Arg Asn Ser Asp Tyr Glu Lys  
 450 455 460  
 Thr Leu Glu Lys Leu Tyr Leu Pro His Ala Tyr Lys Glu Asn Leu Lys  
 465 470 475 480  
 Arg Ala Glu Met Ile Ile Glu Glu Glu Thr Pro Ile Ile Pro Leu Tyr  
 485 490 495  
 50 His Gly Lys Tyr Ile Tyr Ala Ile His Pro Lys Ile Gln Asn Thr Phe  
 500 505 510  
 Gly Ser Leu Leu Gly His Thr Asp Leu Lys Asn Ile Asp Ile Leu Ser  
 515 520 525

&lt;210&gt; 3

&lt;211&gt; 1226

&lt;212&gt; DNA

&lt;213&gt; Chlamydia pneumoniae



&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1123)

&lt;400&gt; 3

ttccagagaa atcctgatcc tgaaaaactt cctgaaacaa ttgctttaac tataacacgg 60

10	gaacctaag catatcctcc aaggacgtta acataccaat ttg cgg ttg gga aat	115
	Leu Arg Leu Gly Asn	
	1 5	
	aag cct atg caa cct ttt atc ttt act tta ctg tgc ttg aca tct ttg	163
	Lys Pro Met Gln Pro Phe Ile Phe Thr Leu Leu Cys Leu Thr Ser Leu	
	10 15 20	
	gtt tct tta gtc gcc ttt gat gct gcg aat gct cgt aaa cgt tgt gcc	211
20	Val Ser Leu Val Ala Phe Asp Ala Ala Asn Ala Arg Lys Arg Cys Ala	
	25 30 35	
	tgt gct caa act ata gaa cgt gga gag aac ttc ttt tcc ata aaa cgc	259
	Cys Ala Gln Thr Ile Glu Arg Gly Glu Asn Phe Phe Ser Ile Lys Arg	
	40 45 50	
	tct gct tgt gct gaa atc gaa tat caa gaa aaa tct cgc cac gcc tca	307
	Ser Ala Cys Ala Glu Ile Glu Tyr Gln Glu Lys Ser Arg His Ala Ser	
	55 60 65	
30	gca att gaa aga atc tca aaa gat aaa ggc aaa gtc act cca aag cag	355
	Ala Ile Glu Arg Ile Ser Lys Asp Lys Gly Lys Val Thr Pro Lys Gln	
	70 75 80 85	
	att gcg aaa gta gct act aag aaa aag caa aga tac cgt tta ttg cag	403
	Ile Ala Lys Val Ala Thr Lys Lys Lys Gln Arg Tyr Arg Leu Leu Gln	
	90 95 100	
	gtt cct ttt tca agg cct ccg aat aac tca agg tat aac ctc tat gct	451
40	Val Pro Phe Ser Arg Pro Pro Asn Asn Ser Arg Tyr Asn Leu Tyr Ala	
	105 110 115	
	ttg ctt agt gaa cct ccc gaa tgc tat agc gat aca gca tca tgg tat	499
	Leu Leu Ser Glu Pro Pro Glu Cys Tyr Ser Asp Thr Ala Ser Trp Tyr	
	120 125 130	
	gct att ttt att cgg tta ctt cga cgt gct tat gta gac acg gga aat	547
	Ala Ile Phe Ile Arg Leu Leu Arg Arg Ala Tyr Val Asp Thr Gly Asn	
	135 140 145	
50	gta cct cct gga tct gag tat gcc atc gct aat gct ttg ata agt aac	595
	Val Pro Pro Gly Ser Glu Tyr Ala Ile Ala Asn Ala Leu Ile Ser Asn	
	150 155 160 165	
	aaa caa gag att tta gag agg gga gcg cag ctt gga ccc gat gtt att	643
	Lys Gln Glu Ile Leu Glu Arg Gly Ala Gln Leu Gly Pro Asp Val Ile	
	170 175 180	
	gaa act cta aca ttg cct gag gaa caa gcc gag att ttt tat aaa atg	691
60	Glu Thr Leu Thr Leu Pro Glu Glu Gln Ala Glu Ile Phe Tyr Lys Met	
	185 190 195	

	ctc	aaa	ggg	tcg	tca	aac	tct	cag	tcg	cta	ctg	aat	ttt	ctg	cat	tat	739
	Leu	Lys	Gly	Ser	Ser	Asn	Ser	Gln	Ser	Leu	Leu	Asn	Phe	Leu	His	Tyr	
			200					205					210				
	gaa	gag	aaa	agc	tta	ggc	cac	tgt	aag	cta	aat	ctg	atc	ttc	atg	gat	787
	Glu	Glu	Lys	Ser	Leu	Gly	His	Cys	Lys	Leu	Asn	Leu	Ile	Phe	Met	Asp	
			215				220					225					
10	ccc	cta	ctg	tta	gaa	gct	gtt	cta	gat	cat	ccc	gat	gct	tat	agg	gaa	835
	Pro	Leu	Leu	Leu	Glu	Ala	Val	Leu	Asp	His	Pro	Asp	Ala	Tyr	Arg	Glu	
						235					240					245	
	acg	tcg	ctc	ctg	cgc	gat	ggc	att	tgg	gaa	gcg	gtg	aag	cgt	caa	gaa	883
	Thr	Ser	Leu	Leu	Arg	Asp	Gly	Ile	Trp	Glu	Ala	Val	Lys	Arg	Gln	Glu	
					250					255					260		
	cat	gcc	atc	caa	gaa	cat	ggc	cag	gca	gct	gct	ttg	gag	ctt	ttt	aaa	931
20	His	Ala	Ile	Gln	Glu	His	Gly	Gln	Ala	Ala	Ala	Leu	Glu	Leu	Phe	Lys	
				265				270						275			
	aca	cgc	acc	gac	ttc	cgc	ctg	gag	ctg	cga	gat	aag	atg	cag	tta	ctt	979
	Thr	Arg	Thr	Asp	Phe	Arg	Leu	Glu	Leu	Arg	Asp	Lys	Met	Gln	Leu	Leu	
			280					285					290				
	cta	agt	cga	tac	gat	ttg	ctc	ccc	tta	tta	aat	aaa	aaa	atg	ttc	gac	1027
	Leu	Ser	Arg	Tyr	Asp	Leu	Leu	Pro	Leu	Leu	Asn	Lys	Lys	Met	Phe	Asp	
			295				300					305					
30	tac	acc	tta	gga	agt	gcc	gga	gat	tac	tta	ttt	ttg	gta	gac	cca	gat	1075
	Tyr	Thr	Leu	Gly	Ser	Ala	Gly	Asp	Tyr	Leu	Phe	Leu	Val	Asp	Pro	Asp	
			310				315				320					325	
	act	aag	gca	att	tct	cga	tgt	cgc	tgc	cct	tca	aag	agt	att	aaa	tta	1123
	Thr	Lys	Ala	Ile	Ser	Arg	Cys	Arg	Cys	Pro	Ser	Lys	Ser	Ile	Lys	Leu	
					330					335					340		
40	taattttaatt	ttaatat	tttta	ttttaaatag	ttttttttga	taattgtctt	aataagtact	1183									
	ataaaaaata	tttctat	agg	taggaccatg	gcagacgaga	ccc	1226										
	<210>	4															
	<211>	341															
	<212>	PRT															
	<213>	Chlamydia	pneumoniae														
	<400>	4															
50	Leu	Arg	Leu	Gly	Asn	Lys	Pro	Met	Gln	Pro	Phe	Ile	Phe	Thr	Leu	Leu	
	1				5					10					15		
	Cys	Leu	Thr	Ser	Leu	Val	Ser	Leu	Val	Ala	Phe	Asp	Ala	Ala	Asn	Ala	
				20					25					30			
	Arg	Lys	Arg	Cys	Ala	Cys	Ala	Gln									

Ser Arg His Ala Ser Ala Ile Glu Arg Ile Ser Lys Asp Lys Gly Lys  
 65 70 75 80  
 Val Thr Pro Lys Gln Ile Ala Lys Val Ala Thr Lys Lys Lys Gln Arg  
 85 90 95  
 Tyr Arg Leu Leu Gln Val Pro Phe Ser Arg Pro Pro Asn Asn Ser Arg  
 10 100 105 110  
 Tyr Asn Leu Tyr Ala Leu Leu Ser Glu Pro Pro Glu Cys Tyr Ser Asp  
 115 120 125  
 Thr Ala Ser Trp Tyr Ala Ile Phe Ile Arg Leu Leu Arg Arg Ala Tyr  
 130 135 140  
 Val Asp Thr Gly Asn Val Pro Pro Gly Ser Glu Tyr Ala Ile Ala Asn  
 145 150 155 160  
 20 Ala Leu Ile Ser Asn Lys Gln Glu Ile Leu Glu Arg Gly Ala Gln Leu  
 165 170 175  
 Gly Pro Asp Val Ile Glu Thr Leu Thr Leu Pro Glu Glu Gln Ala Glu  
 180 185 190  
 Ile Phe Tyr Lys Met Leu Lys Gly Ser Ser Asn Ser Gln Ser Leu Leu  
 195 200 205  
 30 Asn Phe Leu His Tyr Glu Glu Lys Ser Leu Gly His Cys Lys Leu Asn  
 210 215 220  
 Leu Ile Phe Met Asp Pro Leu Leu Leu Glu Ala Val Leu Asp His Pro  
 225 230 235 240  
 Asp Ala Tyr Arg Glu Thr Ser Leu Leu Arg Asp Gly Ile Trp Glu Ala  
 245 250 255  
 Val Lys Arg Gln Glu His Ala Ile Gln Glu His Gly Gln Ala Ala Ala  
 260 265 270  
 40 Leu Glu Leu Phe Lys Thr Arg Thr Asp Phe Arg Leu Glu Leu Arg Asp  
 275 280 285  
 Lys Met Gln Leu Leu Leu Ser Arg Tyr Asp Leu Leu Pro Leu Leu Asn  
 290 295 300  
 Lys Lys Met Phe Asp Tyr Thr Leu Gly Ser Ala Gly Asp Tyr Leu Phe  
 305 310 315 320  
 50 Leu Val Asp Pro Asp Thr Lys Ala Ile Ser Arg Cys Arg Cys Pro Ser  
 325 330 335  
 Lys Ser Ile Lys Leu  
 340

<210> 5  
 <211> 1235  
 60 <212> DNA  
 <213> Chlamydia pneumoniae

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (101)..(1132)

&lt;400&gt; 5

gttactttttt ttttcataaaa aaccccatgt aactttttact tgctcatatt gagaagtccc 60

10	ccatactata aaaggcaacg ttttcttttc ttgggtttttt	atg ctc acc cta ggc	115
		Met Leu Thr Leu Gly	
		1 5	
	ttg gaa agt tct tgc gat gag act gcc tgc gct ata gtt aat gag gat	163	
	Leu Glu Ser Ser Cys Asp Glu Thr Ala Cys Ala Ile Val Asn Glu Asp		
	10 15 20		
	aag cag ata tta gca aat att att gcc tct caa gat atc cat gca tcc	211	
20	Lys Gln Ile Leu Ala Asn Ile Ile Ala Ser Gln Asp Ile His Ala Ser		
	25 30 35		
	tat ggc gga gtc gtt cct gaa ctt gct tca aga gca cat ctc cat atc	259	
	Tyr Gly Gly Val Val Pro Glu Leu Ala Ser Arg Ala His Leu His Ile		
	40 45 50		
	ttc cca caa gtg ata aat aaa gct cta caa cag gcc aac tta ttg atc	307	
	Phe Pro Gln Val Ile Asn Lys Ala Leu Gln Gln Ala Asn Leu Leu Ile		
	55 60 65		
30	gaa gat atg gat ctg att gca gta acg caa act cca ggg ttg ata ggt	355	
	Glu Asp Met Asp Leu Ile Ala Val Thr Gln Thr Pro Gly Leu Ile Gly		
	70 75 80 85		
	tct cta tca gta gga gtg cat ttt ggt aaa ggc att gcc ata gga gca	403	
	Ser Leu Ser Val Gly Val His Phe Gly Lys Gly Ile Ala Ile Gly Ala		
	90 95 100		
	aaa aaa tcc ttg att gga gtc aat cac gtc gaa gct cat ctc tat gct	451	
40	Lys Lys Ser Leu Ile Gly Val Asn His Val Glu Ala His Leu Tyr Ala		
	105 110 115		
	gcc tat atg gca gcg caa aac gtg caa ttc cct gct tta ggt ctt gtg	499	
	Ala Tyr Met Ala Ala Gln Asn Val Gln Phe Pro Ala Leu Gly Leu Val		
	120 125 130		
	gtc tct gga gct cat acc gca gcg ttt ttt ata gaa aat cct aca tcc	547	
	Val Ser Gly Ala His Thr Ala Ala Phe Phe Ile Glu Asn Pro Thr Ser		
	135 140 145		
50	tat aaa ctc ata gga aaa act cga gat gat gct ata gga gaa act ttt	595	
	Tyr Lys Leu Ile Gly Lys Thr Arg Asp Asp Ala Ile Gly Glu Thr Phe		
	150 155 160 165		
	gat aaa gta gga cgc ttt cta gga tta cca tac cct gca ggc cca tta	643	
	Asp Lys Val Gly Arg Phe Leu Gly Leu Pro Tyr Pro Ala Gly Pro Leu		
	170 175 180		
	att gaa aaa ctc gct tta gaa ggc tct gag gac agt tat cct ttt agt	691	
60	Ile Glu Lys Leu Ala Leu Glu Gly Ser Glu Asp Ser Tyr Pro Phe Ser		
	185 190 195		

```

cca gct aaa gtc cca aac tat gac ttt tca ttc agc ggt ctt aaa aca 739
Pro Ala Lys Val Pro Asn Tyr Asp Phe Ser Phe Ser Gly Leu Lys Thr
      200                      205                      210

gct gtt ctc tac gca atc aaa gga aat aat agt agc ccc cgc tct cct 787
Ala Val Leu Tyr Ala Ile Lys Gly Asn Asn Ser Ser Pro Arg Ser Pro
      215                      220                      225

gct cca gag ata tct tta gaa aaa caa aga gat atc gct gct tca ttt 835
Ala Pro Glu Ile Ser Leu Glu Lys Gln Arg Asp Ile Ala Ala Ser Phe
      230                      235                      240                      245

caa aaa gcg gcc tgc act act att gca caa aaa ctt ccc act att ata 883
Gln Lys Ala Ala Cys Thr Thr Ile Ala Gln Lys Leu Pro Thr Ile Ile
      250                      255                      260

aaa gaa ttt tcg tgc cga tct ata ctt att gga ggt ggc gta gcc att 931
Lys Glu Phe Ser Cys Arg Ser Ile Leu Ile Gly Gly Gly Val Ala Ile
      265                      270                      275

aat gaa tac ttt aga tcc gca ata caa act gcg tgt aat cta cct gta 979
Asn Glu Tyr Phe Arg Ser Ala Ile Gln Thr Ala Cys Asn Leu Pro Val
      280                      285                      290

tac ttc ccc cct gct aaa cta tgc tca gat aat gct gct atg att gca 1027
Tyr Phe Pro Pro Ala Lys Leu Cys Ser Asp Asn Ala Ala Met Ile Ala
      295                      300                      305

ggt cta ggg gga gaa aat ttt caa aaa aac tct agt att ccg gaa att 1075
Gly Leu Gly Gly Glu Asn Phe Gln Lys Asn Ser Ser Ile Pro Glu Ile
      310                      315                      320                      325

cgt ata tgc gca aga tat cag tgg gaa tct gta tca cca ttc tcc tta 1123
Arg Ile Cys Ala Arg Tyr Gln Trp Glu Ser Val Ser Pro Phe Ser Leu
      330                      335                      340

gcc tct ccg tagtctcca aggctgcaag gagtccagtc actcctctac 1172
Ala Ser Pro

atctcgggga gaactcgcta ttaatataag agatgaaccc cggtctcttag atccaagaca 1232
agt 1235

```

```

<210> 6
<211> 344
<212> PRT
<213> Chlamydia pneumoniae

```

```

<220>
<221> SITE
<222> (220)...(231)
<223> B-cell epitope

```

```

<220>
<221> SITE
<222> (313)...(321)
<223> B-cell epitope

```

```

<220>
<221> SITE
<222> (67)...(76)
<223> T-cell epitope

<220>
<221> SITE
10 <222> (66)...(75)
    <223> T-cell epitope

<400> 6
Met Leu Thr Leu Gly Leu Glu Ser Ser Cys Asp Glu Thr Ala Cys Ala
   1             5             10             15

Ile Val Asn Glu Asp Lys Gln Ile Leu Ala Asn Ile Ile Ala Ser Gln
          20             25             30

20 Asp Ile His Ala Ser Tyr Gly Gly Val Val Pro Glu Leu Ala Ser Arg
    35             40             45

Ala His Leu His Ile Phe Pro Gln Val Ile Asn Lys Ala Leu Gln Gln
   50             55             60

Ala Asn Leu Leu Ile Glu Asp Met Asp Leu Ile Ala Val Thr Gln Thr
   65             70             75             80

30 Pro Gly Leu Ile Gly Ser Leu Ser Val Gly Val His Phe Gly Lys Gly
    85             90             95

Ile Ala Ile Gly Ala Lys Lys Ser Leu Ile Gly Val Asn His Val Glu
    100            105            110

Ala His Leu Tyr Ala Ala Tyr Met Ala Ala Gln Asn Val Gln Phe Pro
    115            120            125

Ala Leu Gly Leu Val Val Ser Gly Ala His Thr Ala Ala Phe Phe Ile
    130            135            140

40 Glu Asn Pro Thr Ser Tyr Lys Leu Ile Gly Lys Thr Arg Asp Asp Ala
    145            150            155            160

Ile Gly Glu Thr Phe Asp Lys Val Gly Arg Phe Leu Gly Leu Pro Tyr
    165            170            175

Pro Ala Gly Pro Leu Ile Glu Lys Leu Ala Leu Glu Gly Ser Glu Asp
    180            185            190

50 Ser Tyr Pro Phe Ser Pro Ala Lys Val Pro Asn Tyr Asp Phe Ser Phe
    195            200            205

Ser Gly Leu Lys Thr Ala Val Leu Tyr Ala Ile Lys Gly Asn Asn Ser
    210            215            220

Ser Pro Arg Ser Pro Ala Pro Glu Ile Ser Leu Glu Lys Gln Arg Asp
    225            230            235            240

60 Ile Ala Ala Ser Phe Gln Lys Ala Ala Cys Thr Thr Ile Ala Gln Lys
    245            250            255

```

	Leu	Pro	Thr	Ile	Ile	Lys	Glu	Phe	Ser	Cys	Arg	Ser	Ile	Leu	Ile	Gly	
				260					265					270			
	Gly	Gly	Val	Ala	Ile	Asn	Glu	Tyr	Phe	Arg	Ser	Ala	Ile	Gln	Thr	Ala	
			275					280					285				
10	Cys	Asn	Leu	Pro	Val	Tyr	Phe	Pro	Pro	Ala	Lys	Leu	Cys	Ser	Asp	Asn	
		290					295					300					
	Ala	Ala	Met	Ile	Ala	Gly	Leu	Gly	Gly	Glu	Asn	Phe	Gln	Lys	Asn	Ser	
	305					310					315					320	
	Ser	Ile	Pro	Glu	Ile	Arg	Ile	Cys	Ala	Arg	Tyr	Gln	Trp	Glu	Ser	Val	
					325					330					335		
	Ser	Pro	Phe	Ser	Leu	Ala	Ser	Pro									
				340													
20																	
	<210>	7															
	<211>	2060															
	<212>	DNA															
	<213>	Chlamydia pneumoniae															
	<220>																
	<221>	CDS															
	<222>	(101)..(1957)															
30																	
	<400>	7															
	gattttgtgt	atcttttccag	ataatgtttt	taaaaaatg	ttttaaaacc	ctaaaatcct	60										
	acctccttgt	aaccattctc	ggtagaaaag	agagggtattt	atg	aaa	aaa	ggg	aaa							115	
					Met	Lys	Lys	Gly	Lys							5	
										1							
	tta gga gcc	ata gtt ttt	ggc ctt cta	ttt aca agt	agt gtt gct	ggg										163	
	Leu Gly Ala	Ile Val Phe	Gly Leu Leu	Phe Thr Ser	Ser Ser Val	Ala Gly											
			10				15							20			
40																	
	ttt tct aag	gat ttg act	aaa gac aac	gct tat caa	gat tta aat	gtc										211	
	Phe Ser Lys	Asp Leu Thr	Lys Asp Asn	Ala Tyr Gln	Asp Leu Asn	Val											
			25				30						35				
	ata gag cat	tta ata tcg	tta aaa tat	gct cct tta	cca tgg aag	gaa										259	
	Ile Glu His	Leu Ile Ser	Leu Lys Tyr	Ala Pro Leu	Pro Trp Lys	Glu											
			40				45					50					
50																	
	cta tta ttt	ggg tgg gat	tta tct cag	caa aca cag	caa gct cgc	ttg										307	
	Leu Leu Phe	Gly Trp Asp	Leu Ser Gln	Gln Gln Thr	Gln Gln Ala	Arg	Leu										
			55				60					65					
	caa ctg gtc	tta gaa gaa	aaa cca aca	acc aac tac	tgc cag aag	gta										355	
	Gln Leu Val	Leu Glu Glu	Lys Pro Thr	Thr Asn Tyr	Cys Gln Lys	Val											
			70			7											

	ttt tat cgt act gaa agt gcg tat atc cct tac gta ttg aag tta agt	451
	Phe Tyr Arg Thr Glu Ser Ala Tyr Ile Pro Tyr Val Leu Lys Leu Ser	
	105 110 115	
	gaa gat ggt cat gtc ttt gta gtc gac gta cag act agc caa ggg gat	499
	Glu Asp Gly His Val Phe Val Val Asp Val Gln Thr Ser Gln Gly Asp	
	120 125 130	
10	att tac tta ggg gat gaa atc ctt gaa gta gat gga atg ggg att cgt	547
	Ile Tyr Leu Gly Asp Glu Ile Leu Glu Val Asp Gly Met Gly Ile Arg	
	135 140 145	
	gag gct atc gaa agc ctt cgc ttt gga cga ggg agt gcc aca gac tat	595
	Glu Ala Ile Glu Ser Leu Arg Phe Gly Arg Gly Ser Ala Thr Asp Tyr	
	150 155 160 165	
20	tct gct gca gtt cgt tcc ttg aca tcg cgt tcc gcc gct ttt gga gat	643
	Ser Ala Ala Val Arg Ser Leu Thr Ser Arg Ser Ala Ala Phe Gly Asp	
	170 175 180	
	gcg gtt cct tca gga att gcc atg ttg aaa ctt cgc cga ccc agt ggt	691
	Ala Val Pro Ser Gly Ile Ala Met Leu Lys Leu Arg Arg Pro Ser Gly	
	185 190 195	
	ttg atc cgt tcg aca ccg gtc cgt tgg cgt tat act cca gag cat atc	739
	Leu Ile Arg Ser Thr Pro Val Arg Trp Arg Tyr Thr Pro Glu His Ile	
	200 205 210	
30	gga gat ttt tct tta gtt gct cct ttg att cct gaa cat aaa cct caa	787
	Gly Asp Phe Ser Leu Val Ala Pro Leu Ile Pro Glu His Lys Pro Gln	
	215 220 225	
	tta cct aca caa agt tgt gtg cta ttc cgt tcc ggg gta aat tca cag	835
	Leu Pro Thr Gln Ser Cys Val Leu Phe Arg Ser Gly Val Asn Ser Gln	
	230 235 240 245	
40	tct tct agt agc tct tta ttc agt tcc tac atg gtg cct tat ttc tgg	883
	Ser Ser Ser Ser Ser Leu Phe Ser Ser Tyr Met Val Pro Tyr Phe Trp	
	250 255 260	
	gaa gaa ttg cgg gtt caa aat aag cag cgt ttt gac agt aat cac cat	931
	Glu Glu Leu Arg Val Gln Asn Lys Gln Arg Phe Asp Ser Asn His His	
	265 270 275	
	ata ggg agc cgt aat gga ttt tta cct acg ttt ggt cct att ctt tgg	979
	Ile Gly Ser Arg Asn Gly Phe Leu Pro Thr Phe Gly Pro Ile Leu Trp	
	280 285 290	
50	gaa caa gac aag ggg ccc tat cgt tcc tat atc ttt aaa gca aaa gat	1027
	Glu Gln Asp Lys Gly Pro Tyr Arg Ser Tyr Ile Phe Lys Ala Lys Asp	
	295 300 305	
	tct cag ggc aat ccc cat cgc ata gga ttt tta aga att tct tct tat	1075
	Ser Gln Gly Asn Pro His Arg Ile Gly Phe Leu Arg Ile Ser Ser Tyr	
	310 315 320 325	
60	gtt tgg act gat tta gaa gga ctt gaa gag gat cat aag gat agt cct	1123
	Val Trp Thr Asp Leu Glu Gly Leu Glu Glu Asp His Lys Asp Ser Pro	
	330 335 340	



	tgg gag ctc ttt gga gag atc atc gat cat ttg gaa aaa gag act gat	1171
	Trp Glu Leu Phe Gly Glu Ile Ile Asp His Leu Glu Lys Glu Thr Asp	
	345 350 355	
	gct ttg att att gat cag acc cat aat cct gga ggc agt gtt ttc tat	1219
	Ala Leu Ile Ile Asp Gln Thr His Asn Pro Gly Gly Ser Val Phe Tyr	
	360 365 370	
10	ctc tat tcg tta cta tct atg tta aca gat cat cct tta gat act cct	1267
	Leu Tyr Ser Leu Leu Ser Met Leu Thr Asp His Pro Leu Asp Thr Pro	
	375 380 385	
	aaa cat aga atg att ttc act cag gat gaa gtc agc tcg gct ttg cac	1315
	Lys His Arg Met Ile Phe Thr Gln Asp Glu Val Ser Ser Ala Leu His	
	390 395 400 405	
20	tgg caa gat cta cta gaa gat gtc ttc aca gat gag cag gca gtt gcc	1363
	Trp Gln Asp Leu Leu Glu Asp Val Phe Thr Asp Glu Gln Ala Val Ala	
	410 415 420	
	gtg cta ggg gaa act atg gaa gga tat tgc atg gat atg cat gct gta	1411
	Val Leu Gly Glu Thr Met Glu Gly Tyr Cys Met Asp Met His Ala Val	
	425 430 435	
	gcc tct ctt caa aac ttc tct cag agt gtc ctt tct tcc tgg gtt tca	1459
	Ala Ser Leu Gln Asn Phe Ser Gln Ser Val Leu Ser Ser Trp Val Ser	
	440 445 450	
30	ggt gat att aac ctt tca aaa cct atg cct ttg cta gga ttt gca cag	1507
	Gly Asp Ile Asn Leu Ser Lys Pro Met Pro Leu Leu Gly Phe Ala Gln	
	455 460 465	
	gtt cga cct cat cct aaa cat caa tat act aaa cct ttg ttt atg ttg	1555
	Val Arg Pro His Pro Lys His Gln Tyr Thr Lys Pro Leu Phe Met Leu	
	470 475 480 485	
40	ata gac gag gat gac ttc tct tgt gga gat tta gcg cct gca att ttg	1603
	Ile Asp Glu Asp Asp Phe Ser Cys Gly Asp Leu Ala Pro Ala Ile Leu	
	490 495 500	
	aag gat aat ggc cgc gct act ctc att gga aag cca aca gca gga gct	1651
	Lys Asp Asn Gly Arg Ala Thr Leu Ile Gly Lys Pro Thr Ala Gly Ala	
	505 510 515	
	gga ggt ttt gta ttc caa gtc act ttc cct aac cgt tct gga att aaa	1699
	Gly Gly Phe Val Phe Gln Val Thr Phe Pro Asn Arg Ser Gly Ile Lys	
	520 525 530	
50	ggt ctt tct tta aca gga tct tta gct gtt agg aaa gat ggt gag ttt	1747
	Gly Leu Ser Leu Thr Gly Ser Leu Ala Val Arg Lys Asp Gly Glu Phe	
	535 540 545	
	att gaa aac tta gga gtg gct cct cat att gat tta gga ttt acc tcc	1795
	Ile Glu Asn Leu Gly Val Ala Pro His Ile Asp Leu Gly Phe Thr Ser	
	550 555 560 565	
60	agg gat ttg caa act tcc agg ttt act gat tac gtt gag gca gtg aaa	1843
	Arg Asp Leu Gln Thr Ser Arg Phe Thr Asp Tyr Val Glu Ala Val Lys	
	570 575 580	

act ata gtt tta act tct ttg tct gag aac gct aag aag agt gaa gag 1891  
 Thr Ile Val Leu Thr Ser Leu Ser Glu Asn Ala Lys Lys Ser Glu Glu  
 585 590 595

cag act tct ccg caa gag acg cct gaa gtt att cga gtc tct tat ccc 1939  
 Gln Thr Ser Pro Gln Glu Thr Pro Glu Val Ile Arg Val Ser Tyr Pro  
 600 605 610

10 aca acg act tct gct tcg taaacgggac gtaatagaat aatttttatt 1987  
 Thr Thr Thr Ser Ala Ser  
 615

attgctttaa tatgcgcgct tccaatataa gcattgtgaa gcgcgtttca tatgtctttt 2047  
 atcttttagt aat 2060

<210> 8  
 20 <211> 619  
 <212> PRT  
 <213> Chlamydia pneumoniae

<220>  
 <221> SITE  
 <222> (328)...(343)  
 <223> B-cell epitope

<220>  
 30 <221> SITE  
 <222> (589)...(606)  
 <223> B-cell epitope

<220>  
 <221> SITE  
 <222> (135)...(144)  
 <223> T-cell epitope

<220>  
 40 <221> SITE  
 <222> (373)...(382)  
 <223> T-cell epitope

<400> 8  
 Met Lys Lys Gly Lys Leu Gly Ala Ile Val Phe Gly Leu Leu Phe Thr  
 1 5 10 15  
 Ser Ser Val Ala Gly Phe Ser Lys Asp Leu Thr Lys Asp Asn Ala Tyr  
 20 25 30  
 50 Gln Asp Leu Asn Val Ile Glu His Leu Ile Ser Leu Lys Tyr Ala Pro  
 35 40 45  
 Leu Pro Trp Lys Glu Leu Leu Phe Gly Trp Asp Leu Ser Gln Gln Thr  
 50 55 60  
 Gln Gln Ala Arg Leu Gln Leu Val Leu Glu Glu Lys Pro Thr Thr Asn  
 65 70 75 80

60 Tyr Cys Gln Lys Val Leu Ser Asn Tyr Val Arg Ser Leu Asn Asp Tyr  
 85 90 95

	His	Ala	Gly	Ile	Thr	Phe	Tyr	Arg	Thr	Glu	Ser	Ala	Tyr	Ile	Pro	Tyr	
				100					105					110			
	Val	Leu	Lys	Leu	Ser	Glu	Asp	Gly	His	Val	Phe	Val	Val	Asp	Val	Gln	
			115					120					125				
10	Thr	Ser	Gln	Gly	Asp	Ile	Tyr	Leu	Gly	Asp	Glu	Ile	Leu	Glu	Val	Asp	
		130					135					140					
	Gly	Met	Gly	Ile	Arg	Glu	Ala	Ile	Glu	Ser	Leu	Arg	Phe	Gly	Arg	Gly	
	145					150					155					160	
	Ser	Ala	Thr	Asp	Tyr	Ser	Ala	Ala	Val	Arg	Ser	Leu	Thr	Ser	Arg	Ser	
					165					170					175		
	Ala	Ala	Phe	Gly	Asp	Ala	Val	Pro	Ser	Gly	Ile	Ala	Met	Leu	Lys	Leu	
				180					185					190			
20	Arg	Arg	Pro	Ser	Gly	Leu	Ile	Arg	Ser	Thr	Pro	Val	Arg	Trp	Arg	Tyr	
			195					200					205				
	Thr	Pro	Glu	His	Ile	Gly	Asp	Phe	Ser	Leu	Val	Ala	Pro	Leu	Ile	Pro	
		210					215					220					
	Glu	His	Lys	Pro	Gln	Leu	Pro	Thr	Gln	Ser	Cys	Val	Leu	Phe	Arg	Ser	
	225					230					235					240	
30	Gly	Val	Asn	Ser	Gln	Ser	Ser	Ser	Ser	Ser	Leu	Phe	Ser	Ser	Tyr	Met	
					245					250					255		
	Val	Pro	Tyr	Phe	Trp	Glu	Glu	Leu	Arg	Val	Gln	Asn	Lys	Gln	Arg	Phe	
				260					265					270			
	Asp	Ser	Asn	His	His	Ile	Gly	Ser	Arg	Asn	Gly	Phe	Leu	Pro	Thr	Phe	
			275					280					285				
	Gly	Pro	Ile	Leu	Trp	Glu	Gln	Asp	Lys	Gly	Pro	Tyr	Arg	Ser	Tyr	Ile	
40		290					295					300					
	Phe	Lys	Ala	Lys	Asp	Ser	Gln	Gly	Asn	Pro	His	Arg	Ile	Gly	Phe	Leu	
	305					310					315					320	
	Arg	Ile	Ser	Ser	Tyr	Val	Trp	Thr	Asp	Leu	Glu	Gly	Leu	Glu	Glu	Asp	
					325					330					335		
	His	Lys	Asp	Ser	Pro	Trp	Glu	Leu	Phe	Gly	Glu	Ile	Ile	Asp	His	Leu	
				340					345					350			
50	Glu	Lys	Glu	Thr	Asp	Ala	Leu	Ile	Ile	Asp	Gln	Thr	His	Asn	Pro	Gly	
			355					360					365				
	Gly	Ser	Val	Phe	Tyr	Leu	Tyr	Ser	Leu	Leu	Ser	Met	Leu	Thr	Asp	His	
		370					375					380					
	Pro	Leu	Asp	Thr	Pro	Lys	His	Arg	Met	Ile	Phe	Thr	Gln	Asp	Glu	Val	
	385					390					395					400	
60	Ser	Ser	Ala	Leu	His	Trp	Gln	Asp	Leu	Leu	Glu	Asp	Val	Phe	Thr	Asp	
					405					410					415		

	Glu	Gln	Ala	Val	Ala	Val	Leu	Gly	Glu	Thr	Met	Glu	Gly	Tyr	Cys	Met	
				420					425					430			
	Asp	Met	His	Ala	Val	Ala	Ser	Leu	Gln	Asn	Phe	Ser	Gln	Ser	Val	Leu	
			435					440					445				
	Ser	Ser	Trp	Val	Ser	Gly	Asp	Ile	Asn	Leu	Ser	Lys	Pro	Met	Pro	Leu	
10		450					455					460					
	Leu	Gly	Phe	Ala	Gln	Val	Arg	Pro	His	Pro	Lys	His	Gln	Tyr	Thr	Lys	
	465					470					475					480	
	Pro	Leu	Phe	Met	Leu	Ile	Asp	Glu	Asp	Asp	Phe	Ser	Cys	Gly	Asp	Leu	
					485					490					495		
	Ala	Pro	Ala	Ile	Leu	Lys	Asp	Asn	Gly	Arg	Ala	Thr	Leu	Ile	Gly	Lys	
20				500					505					510			
	Pro	Thr	Ala	Gly	Ala	Gly	Gly	Phe	Val	Phe	Gln	Val	Thr	Phe	Pro	Asn	
			515					520					525				
	Arg	Ser	Gly	Ile	Lys	Gly	Leu	Ser	Leu	Thr	Gly	Ser	Leu	Ala	Val	Arg	
		530					535					540					
	Lys	Asp	Gly	Glu	Phe	Ile	Glu	Asn	Leu	Gly	Val	Ala	Pro	His	Ile	Asp	
	545					550					555					560	
30	Leu	Gly	Phe	Thr	Ser	Arg	Asp	Leu	Gln	Thr	Ser	Arg	Phe	Thr	Asp	Tyr	
					565					570					575		
	Val	Glu	Ala	Val	Lys	Thr	Ile	Val	Leu	Thr	Ser	Leu	Ser	Glu	Asn	Ala	
				580					585					590			
	Lys	Lys	Ser	Glu	Glu	Gln	Thr	Ser	Pro	Gln	Glu	Thr	Pro	Glu	Val	Ile	
			595					600					605				
40	Arg	Val	Ser	Tyr	Pro	Thr	Thr	Thr	Ser	Ala	Ser						
		610					615										
	<210>	9															
	<211>	1133															
	<212>	DNA															
	<213>	Chlamydia pneumoniae															
	<220>																
	<221>	CDS															
50	<222>	(101)..(1030)															
	<400>	9															
	gacgtaatag	aataattttt	attattgctt	taatatgcgc	gcttccaata	taagcattgt	60										
	gaagcgcggt	tcatatgtct	tttatcttta	ggtaattatt	atg aga aaa ctt att	115											
					Met Arg Lys Leu Ile												
					1	5											
	tta tgc aat cct aga gga ttt tgc tct gga gtt gtg cgc gct att caa	163															
60	Leu Cys Asn Pro Arg Gly Phe Cys Ser Gly Val Val Arg Ala Ile Gln																
		10							15						20		

	ggt gta gag gtt gct tta gaa aag tgg gga gct cct atc tat gta aaa	211
	Val Val Glu Val Ala Leu Glu Lys Trp Gly Ala Pro Ile Tyr Val Lys	
	25 30 35	
	cat gag att gtt cac aat cgc cat gtt gtt aat gct tta cga gcc aag	259
	His Glu Ile Val His Asn Arg His Val Val Asn Ala Leu Arg Ala Lys	
	40 45 50	
10	gga gcg atc ttt gtt gaa gaa ctt gtt gat gtt cct gaa ggt gag aga	307
	Gly Ala Ile Phe Val Glu Glu Leu Val Asp Val Pro Glu Gly Glu Arg	
	55 60 65	
	gtc att tat tca gct cat gga att cct cct tca gtt aga gct gaa gca	355
	Val Ile Tyr Ser Ala His Gly Ile Pro Pro Ser Val Arg Ala Glu Ala	
	70 75 80 85	
20	aaa gcc cgt aag ctt att gat att gat gct acc tgt ggt ttg gtt act	403
	Lys Ala Arg Lys Leu Ile Asp Ile Asp Ala Thr Cys Gly Leu Val Thr	
	90 95 100	
	aag gtg cat tct gct gcg aag tta tac gca agt aaa gga tac aaa atc	451
	Lys Val His Ser Ala Ala Lys Leu Tyr Ala Ser Lys Gly Tyr Lys Ile	
	105 110 115	
	ata ctg atc ggc cat aag aag cac gtt gag gtg att ggt att gtt gga	499
	Ile Leu Ile Gly His Lys Lys His Val Glu Val Ile Gly Ile Val Gly	
	120 125 130	
30	gaa gtt cct gaa cac att act gtt gtc gag aag gtt gct gac gtc gag	547
	Glu Val Pro Glu His Ile Thr Val Val Glu Lys Val Ala Asp Val Glu	
	135 140 145	
	gcc tta cct ttt agt tct gat aca cct tta ttt tat att act caa acg	595
	Ala Leu Pro Phe Ser Ser Asp Thr Pro Leu Phe Tyr Ile Thr Gln Thr	
	150 155 160 165	
40	acg ttg agt ttg gat gat gtt cag gag atc tca tcg gct ttg cta aag	643
	Thr Leu Ser Leu Asp Asp Val Gln Glu Ile Ser Ser Ala Leu Leu Lys	
	170 175 180	
	cga tat ccc tct atc att act ctg cct agt tct tcg att tgt tat gca	691
	Arg Tyr Pro Ser Ile Ile Thr Leu Pro Ser Ser Ser Ile Cys Tyr Ala	
	185 190 195	
	acc acg aac cgt caa aaa gca ttg cgt tct gtt tta tct cgc gtg aat	739
	Thr Thr Asn Arg Gln Lys Ala Leu Arg Ser Val Leu Ser Arg Val Asn	
	200 205 210	
50	tac gtc tat gtg gtt gga gat gtc aac agc tcg aat tcc aat cgt ctt	787
	Tyr Val Tyr Val Val Gly Asp Val Asn Ser Ser Asn Ser Asn Arg Leu	
	215 220 225	
	cgc gaa gtg gct ttg aga agg gga gtt ccc gct gat ttg atc aac aat	835
	Arg Glu Val Ala Leu Arg Arg Gly Val Pro Ala Asp Leu Ile Asn Asn	
	230 235 240 245	
60	ccc gag gat att gat acg aac atc gta aat cat tct gga gat ata gca	883
	Pro Glu Asp Ile Asp Thr Asn Ile Val Asn His Ser Gly Asp Ile Ala	
	250 255 260	

```

atg act gca gga gcc tca act ccc gaa gac gta gtt caa gct tgc att 931
Met Thr Ala Gly Ala Ser Thr Pro Glu Asp Val Val Gln Ala Cys Ile
      265                      270                      275

cga aag cta tca tca ctt atc cct ggt tta caa gtg gaa aat gat ata 979
Arg Lys Leu Ser Ser Leu Ile Pro Gly Leu Gln Val Glu Asn Asp Ile
      280                      285                      290

10 ttt gct gta gag gat gtc gta ttt caa tta cca aaa gaa ctc cgt tgt 1027
Phe Ala Val Glu Asp Val Val Phe Gln Leu Pro Lys Glu Leu Arg Cys
      295                      300                      305

tct taggtcttta ggcttacttg ccaagttttt ctcgagattg ctttatagag 1080
Ser
310

tcttcttctc gttcagagag ggtatttacc tttttagttc tctgtatttg aaa 1133
20

<210> 10
<211> 310
<212> PRT
<213> Chlamydia pneumoniae

<220>
<221> SITE
<222> (198)...(205)
30 <223> B-cell epitope

<220>
<221> SITE
<222> (221)...(231)
<223> B-cell epitope

<220>
<221> SITE
<222> (207)...(216)
40 <223> T-cell epitope

<220>
<221> SITE
<222> (279)...(288)
<223> T-cell epitope

<220>
<221> SITE
<222> (118)...(127)
50 <223> T-cell epitope

<400> 10
Met Arg Lys Leu Ile Leu Cys Asn Pro Arg Gly Phe Cys Ser Gly Val
  1              5              10              15

Val Arg Ala Ile Gln Val Val Glu Val Ala Leu Glu Lys Trp Gly Ala
      20              25              30

Pro Ile Tyr Val Lys His Glu Ile Val His Asn Arg His Val Val Asn
60      35              40              45

```

Ala Leu Arg Ala Lys Gly Ala Ile Phe Val Glu Glu Leu Val Asp Val  
 50 55 60  
 Pro Glu Gly Glu Arg Val Ile Tyr Ser Ala His Gly Ile Pro Pro Ser  
 65 70 75 80  
 Val Arg Ala Glu Ala Lys Ala Arg Lys Leu Ile Asp Ile Asp Ala Thr  
 10 85 90 95  
 Cys Gly Leu Val Thr Lys Val His Ser Ala Ala Lys Leu Tyr Ala Ser  
 100 105 110  
 Lys Gly Tyr Lys Ile Ile Leu Ile Gly His Lys Lys His Val Glu Val  
 115 120 125  
 Ile Gly Ile Val Gly Glu Val Pro Glu His Ile Thr Val Val Glu Lys  
 130 135 140  
 20 Val Ala Asp Val Glu Ala Leu Pro Phe Ser Ser Asp Thr Pro Leu Phe  
 145 150 155 160  
 Tyr Ile Thr Gln Thr Thr Leu Ser Leu Asp Asp Val Gln Glu Ile Ser  
 165 170 175  
 Ser Ala Leu Leu Lys Arg Tyr Pro Ser Ile Ile Thr Leu Pro Ser Ser  
 180 185 190  
 30 Ser Ile Cys Tyr Ala Thr Thr Asn Arg Gln Lys Ala Leu Arg Ser Val  
 195 200 205  
 Leu Ser Arg Val Asn Tyr Val Tyr Val Val Gly Asp Val Asn Ser Ser  
 210 215 220  
 Asn Ser Asn Arg Leu Arg Glu Val Ala Leu Arg Arg Gly Val Pro Ala  
 225 230 235 240  
 Asp Leu Ile Asn Asn Pro Glu Asp Ile Asp Thr Asn Ile Val Asn His  
 40 245 250 255  
 Ser Gly Asp Ile Ala Met Thr Ala Gly Ala Ser Thr Pro Glu Asp Val  
 260 265 270  
 Val Gln Ala Cys Ile Arg Lys Leu Ser Ser Leu Ile Pro Gly Leu Gln  
 275 280 285  
 Val Glu Asn Asp Ile Phe Ala Val Glu Asp Val Val Phe Gln Leu Pro  
 290 295 300  
 50 Lys Glu Leu Arg Cys Ser  
 305 310

&lt;210&gt; 11

&lt;211&gt; 1466

&lt;212&gt; DNA

&lt;213&gt; Chlamydia pneumoniae

&lt;220&gt;

60 &lt;221&gt; CDS

&lt;222&gt; (101)..(1363)

```

<400> 11
catgggagcc gaggaagcca tctcctacgg acttattgat aaggtggtaa cttctgcgaa 60

agaaactaat aaggatacaa gtagcactta gagagaacat atg aat aaa aaa aat 115
                                         Met Asn Lys Lys Asn
                                         1           5

10  cta act att tgt tca ttt tgc ggt cgg tct gaa aaa gat gta gag aaa 163
    Leu Thr Ile Cys Ser Phe Cys Gly Arg Ser Glu Lys Asp Val Glu Lys
           10           15           20

    ctg att gct ggg cct tcg gta tac att tgt gac tac tgc atc aaa tta 211
    Leu Ile Ala Gly Pro Ser Val Tyr Ile Cys Asp Tyr Cys Ile Lys Leu
           25           30           35

    tgc tct gga att tta gat aag aaa ccc tcc tct aca ata tcc tca gct 259
    Cys Ser Gly Ile Leu Asp Lys Lys Pro Ser Ser Thr Ile Ser Ser Ala
    20           40           45           50

    cca gtt tct gaa aca cct tca cag cct tct gat ctc agg gtg ctt acc 307
    Pro Val Ser Glu Thr Pro Ser Gln Pro Ser Asp Leu Arg Val Leu Thr
           55           60           65

    cct aag gaa atc aaa aag cat att gat gaa tat gtc att ggt cag gaa 355
    Pro Lys Glu Ile Lys Lys His Ile Asp Glu Tyr Val Ile Gly Gln Glu
           70           75           80           85

30  aga gct aaa aag aca atc gct gtt gct gtt tat aat cac tat aaa cgt 403
    Arg Ala Lys Lys Thr Ile Ala Val Ala Val Tyr Asn His Tyr Lys Arg
           90           95           100

    ata cgt gct cta cta cat aac aaa cag gta agc tac ggg aaa tct aac 451
    Ile Arg Ala Leu Leu His Asn Lys Gln Val Ser Tyr Gly Lys Ser Asn
           105           110           115

    gtg ctt ctc cta ggc cct aca gga tct gga aaa aca tta att gca aaa 499
    Val Leu Leu Leu Gly Pro Thr Gly Ser Gly Lys Thr Leu Ile Ala Lys
    40           120           125           130

    aca ttg gca aaa att tta gat gtt ccc ttc acc ata gcc gac gca acg 547
    Thr Leu Ala Lys Ile Leu Asp Val Pro Phe Thr Ile Ala Asp Ala Thr
           135           140           145

    acc cta acg gaa gca ggt tat gtc ggt gaa gat gta gag aac att gtc 595
    Thr Leu Thr Glu Ala Gly Tyr Val Gly Glu Asp Val Glu Asn Ile Val
           150           155           160           165

50  tta cgt tta tta caa gct gct gat tac gat gtc gcc cgt gca gaa cga 643
    Leu Arg Leu Leu Gln Ala Ala Asp Tyr Asp Val Ala Arg Ala Glu Arg
           170           175           180

    ggc att atc tat atc gat gaa atc gat aaa att gga agg aca aca gca 691
    Gly Ile Ile Tyr Ile Asp Glu Ile Asp Lys Ile Gly Arg Thr Thr Ala
           185           190           195

    aac gtc tcc att act aga gat gtt tct ggc gaa ggg gtt caa caa gca 739
    Asn Val Ser Ile Thr Arg Asp Val Ser Gly Glu Gly Val Gln Gln Ala
    60           200           205           210

```



	ttg	tta	aaa	atc	gtt	gaa	gga	acc	aca	gca	aac	gtt	cct	cct	aaa	gga	787
	Leu	Leu	Lys	Ile	Val	Glu	Gly	Thr	Thr	Ala	Asn	Val	Pro	Pro	Lys	Gly	
	215						220					225					
	gga	cgt	aag	cat	cct	aac	caa	gag	tat	atc	cga	gtc	aat	acg	gaa	aat	835
	Gly	Arg	Lys	His	Pro	Asn	Gln	Glu	Tyr	Ile	Arg	Val	Asn	Thr	Glu	Asn	
	230					235					240					245	
10	atc	tta	ttt	atc	gta	ggc	gga	gcc	ttc	gtc	aac	cta	gat	aag	att	atc	883
	Ile	Leu	Phe	Ile	Val	Gly	Gly	Ala	Phe	Val	Asn	Leu	Asp	Lys	Ile	Ile	
					250					255						260	
	gca	aag	cga	ttg	ggg	aaa	act	acc	ata	ggg	ttt	tct	gat	gat	caa	gca	931
	Ala	Lys	Arg	Leu	Gly	Lys	Thr	Thr	Ile	Gly	Phe	Ser	Asp	Asp	Gln	Ala	
				265					270					275			
	gac	ctc	tct	caa	aaa	acc	aga	gac	cat	cta	ctt	gct	aaa	gtt	gaa	acc	979
20	Asp	Leu	Ser	Gln	Lys	Thr	Arg	Asp	His	Leu	Leu	Ala	Lys	Val	Glu	Thr	
			280					285					290				
	gaa	gac	ctg	att	gcc	ttc	gga	atg	atc	cct	gaa	ttt	gtc	gga	aga	ttc	1027
	Glu	Asp	Leu	Ile	Ala	Phe	Gly	Met	Ile	Pro	Glu	Phe	Val	Gly	Arg	Phe	
		295					300					305					
	aac	tgc	att	gta	aac	tgt	gaa	gag	ctt	tct	ttg	gat	gag	ctt	gta	gcc	1075
	Asn	Cys	Ile	Val	Asn	Cys	Glu	Glu	Leu	Ser	Leu	Asp	Glu	Leu	Val	Ala	
30	310					315					320					325	
	atc	ctt	aca	gaa	cct	aca	aat	gcg	att	gtg	aaa	caa	tat	atg	gag	cta	1123
	Ile	Leu	Thr	Glu	Pro	Thr	Asn	Ala	Ile	Val	Lys	Gln	Tyr	Met	Glu	Leu	
					330					335						340	
	ttc	gca	gaa	gaa	aac	gtc	aag	tta	gtc	ttc	aaa	aaa	gaa	gcc	cta	tat	1171
	Phe	Ala	Glu	Glu	Asn	Val	Lys	Leu	Val	Phe	Lys	Lys	Glu	Ala	Leu	Tyr	
				345					350					355			
	gct	ata	gca	aaa	aaa	gcc	aag	caa	gca	aaa	act	gga	gct	cgt	gct	cta	1219
40	Ala	Ile	Ala	Lys	Lys	Ala	Lys	Gln	Ala	Lys	Thr	Gly	Ala	Arg	Ala	Leu	
			360					365					370				
	ggg	atg	atc	cta	gaa	aat	ctc	ctt	aga	gac	ctt	atg	ttt	gaa	att	cct	1267
	Gly	Met	Ile	Leu	Glu	Asn	Leu	Leu	Arg	Asp	Leu	Met	Phe	Glu	Ile	Pro	
		375					380					385					
	tca	gat	cct	aca	gta	gaa	gct	att	cat	atc	caa	gaa	gac	act	atc	gca	1315
	Ser	Asp	Pro	Thr	Val	Glu	Ala	Ile	His	Ile	Gln	Glu	Asp	Thr	Ile	Ala	
	390					395					400					405	
50	gaa	aat	aaa	gcg	cca	ata	att	atc	aga	agg	acc	cca	gaa	gct	atc	gct	1363
	Glu	Asn	Lys	Ala	Pro	Ile	Ile	Ile	Arg	Arg	Thr	Pro	Glu	Al			

60       $\langle 210 \rangle$  12  
          $\langle 211 \rangle$  421

<212> PRT  
 <213> Chlamydia pneumoniae  
  
 <220>  
 <221> SITE  
 <222> (226)...(239)  
 <223> B-cell epitope  
 10  
  
 <220>  
 <221> SITE  
 <222> (273)...(286)  
 <223> B-cell epitope  
  
 <220>  
 <221> SITE  
 <222> (137)...(146)  
 <223> T-cell epitope  
 20  
  
 <220>  
 <221> SITE  
 <222> (168)...(177)  
 <223> T-cell epitope  
  
 <400> 12  
 Met Asn Lys Lys Asn Leu Thr Ile Cys Ser Phe Cys Gly Arg Ser Glu  
     1                    5                    10                    15  
 30 Lys Asp Val Glu Lys Leu Ile Ala Gly Pro Ser Val Tyr Ile Cys Asp  
                     20                    25                    30  
 Tyr Cys Ile Lys Leu Cys Ser Gly Ile Leu Asp Lys Lys Pro Ser Ser  
                     35                    40                    45  
 Thr Ile Ser Ser Ala Pro Val Ser Glu Thr Pro Ser Gln Pro Ser Asp  
                     50                    55                    60  
 40 Leu Arg Val Leu Thr Pro Lys Glu Ile Lys Lys His Ile Asp Glu Tyr  
                     65                    70                    75                    80  
 Val Ile Gly Gln Glu Arg Ala Lys Lys Thr Ile Ala Val Ala Val Tyr  
                     85                    90                    95  
 Asn His Tyr Lys Arg Ile Arg Ala Leu Leu His Asn Lys Gln Val Ser  
                     100                    105                    110  
 Tyr Gly Lys Ser Asn Val Leu Leu Leu Gly Pro Thr Gly Ser Gly Lys  
                     115                    120                    125  
 50 Thr Leu Ile Ala Lys Thr Leu Ala Lys Ile Leu Asp Val Pro Phe Thr  
                     130                    135                    140  
 Ile Ala Asp Ala Thr Thr Leu Thr Glu Ala Gly Tyr Val Gly Glu Asp  
                     145                    150                    155                    160  
 Val Glu Asn Ile Val Leu Arg Leu Leu Gln Ala Ala Asp Tyr Asp Val  
                     165                    170                    175  
 60 Ala Arg Ala Glu Arg Gly Ile Ile Tyr Ile Asp Glu Ile Asp Lys Ile  
                     180                    185                    190

Gly Arg Thr Thr Ala Asn Val Ser Ile Thr Arg Asp Val Ser Gly Glu  
 195 200 205  
 Gly Val Gln Gln Ala Leu Leu Lys Ile Val Glu Gly Thr Thr Ala Asn  
 210 215 220  
 10 Val Pro Pro Lys Gly Gly Arg Lys His Pro Asn Gln Glu Tyr Ile Arg  
 225 230 235 240  
 Val Asn Thr Glu Asn Ile Leu Phe Ile Val Gly Gly Ala Phe Val Asn  
 245 250 255  
 Leu Asp Lys Ile Ile Ala Lys Arg Leu Gly Lys Thr Thr Ile Gly Phe  
 260 265 270  
 Ser Asp Asp Gln Ala Asp Leu Ser Gln Lys Thr Arg Asp His Leu Leu  
 275 280 285  
 20 Ala Lys Val Glu Thr Glu Asp Leu Ile Ala Phe Gly Met Ile Pro Glu  
 290 295 300  
 Phe Val Gly Arg Phe Asn Cys Ile Val Asn Cys Glu Glu Leu Ser Leu  
 305 310 315 320  
 Asp Glu Leu Val Ala Ile Leu Thr Glu Pro Thr Asn Ala Ile Val Lys  
 325 330 335  
 30 Gln Tyr Met Glu Leu Phe Ala Glu Glu Asn Val Lys Leu Val Phe Lys  
 340 345 350  
 Lys Glu Ala Leu Tyr Ala Ile Ala Lys Lys Ala Lys Gln Ala Lys Thr  
 355 360 365  
 Gly Ala Arg Ala Leu Gly Met Ile Leu Glu Asn Leu Leu Arg Asp Leu  
 370 375 380  
 Met Phe Glu Ile Pro Ser Asp Pro Thr Val Glu Ala Ile His Ile Gln  
 385 390 395 400  
 40 Glu Asp Thr Ile Ala Glu Asn Lys Ala Pro Ile Ile Ile Arg Arg Thr  
 405 410 415  
 Pro Glu Ala Ile Ala  
 420  
 50 <210> 13  
 <211> 812  
 <212> DNA  
 <213> Chlamydia pneumoniae  
 <220>  
 <221> CDS  
 <222> (101) .. (709)  
 <400> 13  
 tgacgtagac agcctaaaaa gtcttagcta cgttcctagg gtcatttcgt gatcggaac 60

```

gtatggacac aactgaaaat tatttgatga ggaaacgcaa atg aca ctg gta ccc 115
                                         Met Thr Leu Val Pro
                                         1           5

tat gtt gtc gag gat acg ggc cgt ggt gaa agg gcc atg gat att tac 163
Tyr Val Val Glu Asp Thr Gly Arg Gly Glu Arg Ala Met Asp Ile Tyr
                        10           15           20

10 tcc cgt ctt ctg aaa gat cgt att gta atg atc ggt cag gaa atc acg 211
Ser Arg Leu Leu Lys Asp Arg Ile Val Met Ile Gly Gln Glu Ile Thr
                        25           30           35

gag ccc ctc gca aac aca gta att gcc cag ctc ctt ttc ctc atg tcc 259
Glu Pro Leu Ala Asn Thr Val Ile Ala Gln Leu Leu Phe Leu Met Ser
                        40           45           50

20 gaa gat cct aaa aag gat att caa att ttc atc aat tcc cca ggc ggc 307
Glu Asp Pro Lys Lys Asp Ile Gln Ile Phe Ile Asn Ser Pro Gly Gly
                        55           60           65

tac atc acc gct gga ctg gca atc tat gat acc att cgc ttt tta ggt 355
Tyr Ile Thr Ala Gly Leu Ala Ile Tyr Asp Thr Ile Arg Phe Leu Gly
                        70           75           80           85

tgt gat gta aat acc tac tgc atc ggt caa gct gca tcc atg gga gcc 403
Cys Asp Val Asn Thr Tyr Cys Ile Gly Gln Ala Ala Ser Met Gly Ala
                        90           95           100

30 ctc tta tta tcc gca gga act aaa gga aag cgt cac gct ctt ccc cat 451
Leu Leu Leu Ser Ala Gly Thr Lys Gly Lys Arg His Ala Leu Pro His
                        105           110           115

agc cgt atg atg atc cac caa cct tct gga ggc att atc gga aca tcc 499
Ser Arg Met Met Ile His Gln Pro Ser Gly Gly Ile Ile Gly Thr Ser
                        120           125           130

40 gca gac atc caa ctc caa gca gct gaa att cta aca cta aaa aaa cac 547
Ala Asp Ile Gln Leu Gln Ala Ala Glu Ile Leu Thr Leu Lys Lys His
                        135           140           145

ctt gcc aat atc ctc tct gaa tgc aca gga caa cct gta gaa aaa att 595
Leu Ala Asn Ile Leu Ser Glu Cys Thr Gly Gln Pro Val Glu Lys Ile
                        150           155           160           165

ata gaa gat tct gaa cga gat ttc ttc atg gga gcc gag gaa gcc atc 643
Ile Glu Asp Ser Glu Arg Asp Phe Phe Met Gly Ala Glu Glu Ala Ile
                        170           175           180

50 tcc tac gga ctt att gat aag gtg gta act tct gcg aaa gaa act aat 691
Ser Tyr Gly Leu Ile Asp Lys Val Val Thr Ser Ala Lys Glu Thr Asn
                        185           190           195

aag gat aca agt agc act tagagagaac atatgaataa aaaaaatcta 739
Lys Asp Thr Ser Ser Thr
                        200

actatttggt cattttgcgg tcggtctgaa aaagatgtag agaaactgat tgctgggcct 799
tcggtataca ttt
60
                        812

```

<210> 14  
 <211> 203  
 <212> PRT  
 <213> Chlamydia pneumoniae  
  
 <220>  
 <221> SITE  
 10 <222> (107)...(116)  
 <223> B-cell epitope  
  
 <220>  
 <221> SITE  
 <222> (193)...(203)  
 <223> B-cell epitope  
  
 <220>  
 <221> SITE  
 20 <222> (76)...(85)  
 <223> T-cell epitope  
  
 <400> 14  
 Met Thr Leu Val Pro Tyr Val Val Glu Asp Thr Gly Arg Gly Glu Arg  
     1                    5                    10                    15  
  
 Ala Met Asp Ile Tyr Ser Arg Leu Leu Lys Asp Arg Ile Val Met Ile  
                     20                    25                    30  
  
 30 Gly Gln Glu Ile Thr Glu Pro Leu Ala Asn Thr Val Ile Ala Gln Leu  
                     35                    40                    45  
  
 Leu Phe Leu Met Ser Glu Asp Pro Lys Lys Asp Ile Gln Ile Phe Ile  
     50                    55                    60  
  
 Asn Ser Pro Gly Gly Tyr Ile Thr Ala Gly Leu Ala Ile Tyr Asp Thr  
     65                    70                    75                    80  
  
 40 Ile Arg Phe Leu Gly Cys Asp Val Asn Thr Tyr Cys Ile Gly Gln Ala  
                     85                    90                    95  
  
 Ala Ser Met Gly Ala Leu Leu Leu Ser Ala Gly Thr Lys Gly Lys Arg  
                     100                    105                    110  
  
 His Ala Leu Pro His Ser Arg Met Met Ile His Gln Pro Ser Gly Gly  
                     115                    120                    125  
  
 Ile Ile Gly Thr Ser Ala Asp Ile Gln Leu Gln Ala Ala Glu Ile Leu  
     130                    135                    140  
  
 50 Thr Leu Lys Lys His Leu Ala Asn Ile Leu Ser Glu Cys Thr Gly Gln  
     145                    150                    155                    160  
  
 Pro Val Glu Lys Ile Ile Glu Asp Ser Glu Arg Asp Phe Phe Met Gly  
                     165                    170                    175  
  
 Ala Glu Glu Ala Ile Ser Tyr Gly Leu Ile Asp Lys Val Val Thr Ser  
                     180                    185                    190  
  
 60 Ala Lys Glu Thr Asn Lys Asp Thr Ser Ser Thr  
     195                    200

	<210>	15	
	<211>	2162	
	<212>	DNA	
	<213>	Chlamydia pneumoniae	
	<220>		
	<221>	CDS	
10	<222>	(101)..(2059)	
	<400>	15	
	gataaaatag aaagacctga tcatttgatg gaaatagcag ctcttcccgga ataccaatat		60
	ttggaatatc cctcagaaga aagtatcagt cttttatcct atg agc tac cgt aaa		115
		Met Ser Tyr Arg Lys	
		1 5	
20	cgt tgc act cta att gtt cta gga gtg ttt gct ctt tat gct ctt cta	163	
	Arg Ser Thr Leu Ile Val Leu Gly Val Phe Ala Leu Tyr Ala Leu Leu		
		10 15 20	
	gta ttg cgt tat tat aaa att caa att tgt gaa gga gac cac tgg gcc		211
	Val Leu Arg Tyr Tyr Lys Ile Gln Ile Cys Glu Gly Asp His Trp Ala		
		25 30 35	
	gca gaa gct ctc ggg caa cac gaa ttt tgt gtc cgt gat cct ttt cga		259
	Ala Glu Ala Leu Gly Gln His Glu Phe Cys Val Arg Asp Pro Phe Arg		
		40 45 50	
30	agg ggc acc ttt ttt gct aac acg aca gta cgt aag gga gac aaa gac	307	
	Arg Gly Thr Phe Phe Ala Asn Thr Thr Val Arg Lys Gly Asp Lys Asp		
		55 60 65	
	ctt cag cag cct ttc gct gtc gat att aca aaa ttt cac ctt tgt gca		355
	Leu Gln Gln Pro Phe Ala Val Asp Ile Thr Lys Phe His Leu Cys Ala		
		70 75 80 85	
40	gat cct tta gct att ccc gaa tgt cat cgt gat gag atc atc caa ggg	403	
	Asp Pro Leu Ala Ile Pro Glu Cys His Arg Asp Glu Ile Ile Gln Gly		
		90 95 100	
	att ctc caa ttt att gag ggg cag acc tac gac gac ctc tcc cta aag		451
	Ile Leu Gln Phe Ile Glu Gly Gln Thr Tyr Asp Asp Leu Ser Leu Lys		
		105 110 115	
	tta gat aag aaa tct cggtat tgt aag ctgtat cct tta tta gat gtt		499
	Leu Asp Lys Lys Ser Arg Tyr Cys Lys Leu Tyr Pro Leu Leu Asp Val		
		120 125 130	
50	tct gtc cat gac cgg cta tcc ctt tgg tgg aaa gga tat gca aca aag	547	
	Ser Val His Asp Arg Leu Ser Leu Trp Trp Lys Gly Tyr Ala Thr Lys		
		135 140 145	
	cat cgc tta cca aca aac gcc cta ttt ttt att acg gac tac caa cgc		595
	His Arg Leu Pro Thr Asn Ala Leu Phe Phe Ile Thr Asp Tyr Gln Arg		
		150 155 160 165	
60	tcg tat cct ttt ggg aag ctc ctt gga caa gtt ctc cat acc tta aga	643	
	Ser Tyr Pro Phe Gly Lys Leu Leu Gly Gln Val Leu His Thr Leu Arg		
		170 175 180	

[illegible]

	agt	gag	gcc	tct	ggg	ttg	gtg	cct	tct	ccc	cat	cgt	ttc	cat	att	aat	1411
	Ser	Glu	Ala	Ser	Gly	Leu	Val	Pro	Ser	Pro	His	Arg	Phe	His	Ile	Asn	
				425					430				435				
	ggg	tcc	ctg	gaa	tgg	tcc	tta	tct	act	cca	tat	tct	ttg	gct	atg	gga	1459
	Gly	Ser	Leu	Glu	Trp	Ser	Leu	Ser	Thr	Pro	Tyr	Ser	Leu	Ala	Met	Gly	
				440				445					450				
10	tat	aat	att	ttg	gca	aca	ggg	ata	caa	atg	gtt	caa	gcc	tac	gct	atc	1507
	Tyr	Asn	Ile	Leu	Ala	Thr	Gly	Ile	Gln	Met	Val	Gln	Ala	Tyr	Ala	Ile	
				455			460					465					
	ctt	gca	aac	gga	ggg	tat	gcc	gtc	cgg	ccc	act	tta	gta	aaa	aag	atc	1555
	Leu	Ala	Asn	Gly	Gly	Tyr	Ala	Val	Arg	Pro	Thr	Leu	Val	Lys	Lys	Ile	
				470		475					480					485	
20	gtc	tct	gct	tca	gga	gag	gaa	tat	cat	ctt	cct	act	aaa	gag	aag	aca	1603
	Val	Ser	Ala	Ser	Gly	Glu	Glu	Tyr	His	Leu	Pro	Thr	Lys	Glu	Lys	Thr	
				490						495					500		
	cga	ctc	ttt	tca	gaa	gaa	att	act	aga	gaa	gtt	gtt	cgt	gcc	atg	cgt	1651
	Arg	Leu	Phe	Ser	Glu	Glu	Ile	Thr	Arg	Glu	Val	Val	Arg	Ala	Met	Arg	
				505					510					515			
	ttt	aca	acg	tta	ccc	gga	ggg	tcg	gga	ttt	cga	gcc	tct	cct	aag	cat	1699
	Phe	Thr	Thr	Leu	Pro	Gly	Gly	Ser	Gly	Phe	Arg	Ala	Ser	Pro	Lys	His	
				520				525					530				
30	cac	tct	agt	gct	ggg	aaa	aca	gga	act	aca	gaa	aag	atg	att	cat	gga	1747
	His	Ser	Ser	Ala	Gly	Lys	Thr	Gly	Thr	Thr	Glu	Lys	Met	Ile	His	Gly	
				535			540					545					
	aaa	tat	gat	aaa	cgc	cgt	cat	att	gct	tct	ttt	ata	ggg	ttt	act	ccc	1795
	Lys	Tyr	Asp	Lys	Arg	Arg	His	Ile	Ala	Ser	Phe	Ile	Gly	Phe	Thr	Pro	
				550		555					560					565	
40	gta	gag	agc	tcg	gag	gga	aat	ttc	cca	cct	tta	gtg	atg	ctc	gtc	tcc	1843
	Val	Glu	Ser	Ser	Glu	Gly	Asn	Phe	Pro	Pro	Leu	Val	Met	Leu	Val	Ser	
				570						575					580		
	ata	gat	gat	cct	gaa	tat	ggg	ttg	cga	gcc	gac	ggc	acg	aaa	aat	tat	1891
	Ile	Asp	Asp	Pro	Glu	Tyr	Gly	Leu	Arg	Ala	Asp	Gly	Thr	Lys	Asn	Tyr	
				585					590					595			
	atg	ggg	ggg	cgt	tgt	gcg	gca	ccc	att	ttt	tct	agg	gtt	gct	gac	cgc	1939
	Met	Gly	Gly	Arg	Cys	Ala	Ala	Pro	Ile	Phe	Ser	Arg	Val	Ala	Asp	Arg	
				600			605						610				
50	aca	ctc	ctc	tat	tta	ggg	att	ctt	cca	gac	aag	aag	cta	aga	aat	tgc	1987
	Thr	Leu	Leu	Tyr	Leu	Gly	Ile	Leu	Pro	Asp	Lys	Lys	Leu	Arg	Asn	Cys	



```

cttttaccgt tgagcaaaga ctctctatca gagagcccggt ctctctcttta tcctctatga 2149
gtagtttatg tta 2162

<210> 16
<211> 653
<212> PRT
10 <213> Chlamydia pneumoniae

<220>
<221> SITE
<222> (287)...(306)
<223> B-cell epitope

<220>
<221> SITE
20 <222> (637)...(653)
<223> B-cell epitope

<220>
<221> SITE
<222> (40)...(48)
<223> T-cell epitope

<220>
<221> SITE
30 <222> (456)...(465)
<223> T-cell epitope

<400> 16
Met Ser Tyr Arg Lys Arg Ser Thr Leu Ile Val Leu Gly Val Phe Ala
  1             5             10             15

Leu Tyr Ala Leu Leu Val Leu Arg Tyr Tyr Lys Ile Gln Ile Cys Glu
             20             25             30

Gly Asp His Trp Ala Ala Glu Ala Leu Gly Gln His Glu Phe Cys Val
40             35             40             45

Arg Asp Pro Phe Arg Arg Gly Thr Phe Phe Ala Asn Thr Thr Val Arg
             50             55             60

Lys Gly Asp Lys Asp Leu Gln Gln Pro Phe Ala Val Asp Ile Thr Lys
65             70             75             80

Phe His Leu Cys Ala Asp Pro Leu Ala Ile Pro Glu Cys His Arg Asp
             85             90             95
50

Glu Ile Ile Gln Gly Ile Leu Gln Phe Ile Glu Gly Gln Thr Tyr Asp
             100            105            110

Asp Leu Ser Leu Lys Leu Asp Lys Lys Ser Arg Tyr Cys Lys Leu Tyr
             115            120            125

Pro Leu Leu Asp Val Ser Val His Asp Arg Leu Ser Leu Trp Trp Lys
             130            135            140

60 Gly Tyr Ala Thr Lys His Arg Leu Pro Thr Asn Ala Leu Phe Phe Ile
145             150             155             160

```

Thr Asp Tyr Gln Arg Ser Tyr Pro Phe Gly Lys Leu Leu Gly Gln Val  
 165 170 175  
 Leu His Thr Leu Arg Glu Ile Lys Asp Glu Lys Thr Gly Lys Ala Phe  
 180 185 190  
 10 Pro Thr Gly Gly Met Glu Ala Tyr Phe Asn His Ile Leu Glu Gly Asp  
 195 200 205  
 Val Gly Glu Arg Lys Leu Leu Arg Ser Pro Leu Asn Arg Leu Asp Thr  
 210 215 220  
 Asn Arg Val Ile Lys Leu Pro Lys Asp Gly Ser Asp Ile Tyr Leu Thr  
 225 230 235 240  
 Ile Asn Pro Val Ile Gln Thr Ile Ala Glu Glu Glu Leu Glu Arg Gly  
 245 250 255  
 20 Val Leu Glu Ala Lys Ala Gln Gly Gly Arg Leu Ile Leu Met Asn Ser  
 260 265 270  
 Gln Thr Gly Glu Ile Leu Ala Leu Ala Gln Tyr Pro Phe Phe Asp Pro  
 275 280 285  
 Thr Asn Tyr Lys Glu Tyr Phe Asn Asn Lys Glu Arg Ile Glu His Thr  
 290 295 300  
 30 Lys Val Ser Phe Val Ser Asp Val Phe Glu Pro Gly Ser Ile Met Lys  
 305 310 315 320  
 Pro Leu Thr Val Ala Ile Ala Leu Gln Ala Asn Glu Glu Ala Ser Leu  
 325 330 335  
 Lys Ser Gln Lys Lys Ile Phe Asp Pro Glu Glu Pro Ile Asp Val Thr  
 340 345 350  
 Arg Thr Leu Phe Pro Gly Arg Lys Gly Ser Pro Leu Lys Asp Ile Ser  
 355 360 365  
 40 Arg Asn Ser Gln Leu Asn Met Tyr Met Ala Ile Gln Lys Ser Ser Asn  
 370 375 380  
 Val Tyr Val Ala Gln Leu Ala Asp Arg Ile Ile Gln Ser Leu Gly Val  
 385 390 395 400  
 Ala Trp Tyr Gln Gln Lys Leu Leu Ala Leu Gly Phe Gly Arg Lys Thr  
 405 410 415  
 50 Gly Ile Glu Leu Pro Ser Glu Ala Ser Gly Leu Val Pro Ser Pro His  
 420 425 430  
 Arg Phe His Ile Asn Gly Ser Leu Glu Trp Ser Leu Ser Thr Pro Tyr  
 435 440 445  
 Ser Leu Ala Met Gly Tyr Asn Ile Leu Ala Thr Gly Ile Gln Met Val  
 450 455 460  
 60 Gln Ala Tyr Ala Ile Leu Ala Asn Gly Gly Tyr Ala Val Arg Pro Thr  
 465 470 475 480

Leu Val Lys Lys Ile Val Ser Ala Ser Gly Glu Glu Tyr His Leu Pro  
 485 490 495  
 Thr Lys Glu Lys Thr Arg Leu Phe Ser Glu Glu Ile Thr Arg Glu Val  
 500 505 510  
 10 Val Arg Ala Met Arg Phe Thr Thr Leu Pro Gly Gly Ser Gly Phe Arg  
 515 520 525  
 Ala Ser Pro Lys His His Ser Ser Ala Gly Lys Thr Gly Thr Thr Glu  
 530 535 540  
 Lys Met Ile His Gly Lys Tyr Asp Lys Arg Arg His Ile Ala Ser Phe  
 545 550 555 560  
 Ile Gly Phe Thr Pro Val Glu Ser Ser Glu Gly Asn Phe Pro Pro Leu  
 565 570 575  
 20 Val Met Leu Val Ser Ile Asp Asp Pro Glu Tyr Gly Leu Arg Ala Asp  
 580 585 590  
 Gly Thr Lys Asn Tyr Met Gly Gly Arg Cys Ala Ala Pro Ile Phe Ser  
 595 600 605  
 Arg Val Ala Asp Arg Thr Leu Leu Tyr Leu Gly Ile Leu Pro Asp Lys  
 610 615 620  
 30 Lys Leu Arg Asn Cys Asp Glu Glu Ala Ala Ala Leu Lys Arg Leu Tyr  
 625 630 635 640  
 Glu Glu Trp Asn Arg Ser Pro Lys Gln Gly Gly Thr Arg  
 645 650  
  
 <210> 17  
 <211> 2738  
 <212> DNA  
 40 <213> Chlamydia pneumoniae  
  
 <220>  
 <221> CDS  
 <222> (101)..(2635)  
  
 <400> 17  
 gaattttacc aaatttgctg gtttagagcg aagagttgca tcattatattt aaatttcgta 60  
 tatgcttaag gaaagttcta cccctgtctt ttaggttttt atg ttt gag aag ttc 115  
 50 Met Phe Glu Lys Phe  
 1 5  
 act aat aga gca aaa caa gtc att aaa ctg gcg aaa aag gag gct cag 163  
 Thr Asn Arg Ala Lys Gln Val Ile Lys Leu Ala Lys Lys Glu Ala Gln  
 10 15 20  
 cgt tta aat cat aac tac ctg ggt act gag cac atc ctg ctt ggt ctt 211  
 Arg Leu Asn His Asn Tyr Leu Gly Thr Glu His Ile Leu Leu Gly Leu  
 25 30 35  
 60

	ctc aaa ctt ggt caa ggg gta gct gtt aat gta tta cgc aac ctc ggt	259
	Leu Lys Leu Gly Gln Gly Val Ala Val Asn Val Leu Arg Asn Leu Gly	
	40 45 50	
	ata gat ttt gat acg gca cgg caa gag gtg gaa cgc ctg att ggt tat	307
	Ile Asp Phe Asp Thr Ala Arg Gln Glu Val Glu Arg Leu Ile Gly Tyr	
	55 60 65	
10	ggg cca gaa att caa gtc tac gga gac cct gcc ctt aca gga aga gta	355
	Gly Pro Glu Ile Gln Val Tyr Gly Asp Pro Ala Leu Thr Gly Arg Val	
	70 75 80 85	
	aaa aaa tct ttt gaa tca gca aat gaa gag gcc agc ctt tta gag cac	403
	Lys Lys Ser Phe Glu Ser Ala Asn Glu Glu Ala Ser Leu Leu Glu His	
	90 95 100	
20	aat tat gtc ggg acg gag cat tta ctc tta ggg atc cta cat caa tca	451
	Asn Tyr Val Gly Thr Glu His Leu Leu Leu Gly Ile Leu His Gln Ser	
	105 110 115	
	gat agt gtc gct ctt cag gta tta gaa aac tta cat atc gat cca aga	499
	Asp Ser Val Ala Leu Gln Val Leu Glu Asn Leu His Ile Asp Pro Arg	
	120 125 130	
	gag gtt cgt aag gaa att ctt aga gaa tta gag acc ttc aat cta caa	547
	Glu Val Arg Lys Glu Ile Leu Arg Glu Leu Glu Thr Phe Asn Leu Gln	
	135 140 145	
30	ctt cct cct tcg tcg tcg tct tct tcc tca tcc tct cga agc aac cct	595
	Leu Pro Pro Ser Ser Ser Ser Ser Ser Ser Ser Ser Arg Ser Asn Pro	
	150 155 160 165	
	tca tct tca aaa tct cct tta ggt cat agc tta ggt tct gac aaa aac	643
	Ser Ser Ser Lys Ser Pro Leu Gly His Ser Leu Gly Ser Asp Lys Asn	
	170 175 180	
40	gaa aag ctt tct gct ctg aaa gca tat ggt tat gat tta acg gag atg	691
	Glu Lys Leu Ser Ala Leu Lys Ala Tyr Gly Tyr Asp Leu Thr Glu Met	
	185 190 195	
	gtc cga gag tct aag ctc gat cct gtc att ggt cgt tct tca gaa gtc	739
	Val Arg Glu Ser Lys Leu Asp Pro Val Ile Gly Arg Ser Ser Glu Val	
	200 205 210	
	gaa cgg ttg att ttg att ctt tgc cga aga aga aaa aac aat cct gta	787
	Glu Arg Leu Ile Leu Ile Leu Cys Arg Arg Arg Lys Asn Asn Pro Val	
	215 220 225	
50	ctt att gga gaa gct gga gtt ggt aag act gca att gtt gag ggt ctg	835
	Leu Ile Gly Glu Ala Gly Val Gly Lys Thr Ala Ile Val Glu Gly Leu	
	230 235 240 245	
	gct caa aaa atc att ctg aat gag gtt cct gat gcc tta cgg aaa aag	883
	Ala Gln Lys Ile Ile Leu Asn Glu Val Pro Asp Ala Leu Arg Lys Lys	
	250 255 260	
60	cga ctg att act cta gat cta gca tta atg att gct gga aca aaa tat	931
	Arg Leu Ile Thr Leu Asp Leu Ala Leu Met Ile Ala Gly Thr Lys Tyr	
	265 270 275	

	cga ggg caa ttt gag gaa cgg atc aaa gct gtc atg gat gaa gtt cgc	979
	Arg Gly Gln Phe Glu Glu Arg Ile Lys Ala Val Met Asp Glu Val Arg	
	280 285 290	
	aag cat gga aac atc ttg ctc ttc att gac gag ctc cac acg att gta	1027
	Lys His Gly Asn Ile Leu Leu Phe Ile Asp Glu Leu His Thr Ile Val	
	295 300 305	
10	gga gca gga gca gct gaa ggt gct atc gat gct tca aac att tta aaa	1075
	Gly Ala Gly Ala Ala Glu Gly Ala Ile Asp Ala Ser Asn Ile Leu Lys	
	310 315 320 325	
	cct gcg tta gcg cga ggt gaa att cag tgt att gga gca act acg ata	1123
	Pro Ala Leu Ala Arg Gly Glu Ile Gln Cys Ile Gly Ala Thr Thr Ile	
	330 335 340	
20	gat gag tat cgc aag cac ata gaa aaa gac gca gct tta gaa cgt cgt	1171
	Asp Glu Tyr Arg Lys His Ile Glu Lys Asp Ala Ala Leu Glu Arg Arg	
	345 350 355	
	ttc caa aaa atc gtg gtt cac cct cct agt gta gat gag act att gag	1219
	Phe Gln Lys Ile Val Val His Pro Pro Ser Val Asp Glu Thr Ile Glu	
	360 365 370	
	att tta cgt ggc ctc aag aaa aag tat gaa gaa cat cac aat gtc ttc	1267
	Ile Leu Arg Gly Leu Lys Lys Lys Tyr Glu Glu His His Asn Val Phe	
	375 380 385	
30	att act gaa gaa gct tta aaa gca gct gcg act ctt tct gat caa tat	1315
	Ile Thr Glu Glu Ala Leu Lys Ala Ala Ala Thr Leu Ser Asp Gln Tyr	
	390 395 400 405	
	gtt cat gga cgt ttc ctc cct gat aaa gca ata gat ctt tta gat gaa	1363
	Val His Gly Arg Phe Leu Pro Asp Lys Ala Ile Asp Leu Leu Asp Glu	
	410 415 420	
40	gct ggg gct cgt gtc cgt gtg aat aca atg ggt cag cct aca gat tta	1411
	Ala Gly Ala Arg Val Arg Val Asn Thr Met Gly Gln Pro Thr Asp Leu	
	425 430 435	
	atg aag cta gag gct gaa atc gaa aat aca aaa ttg gcc aaa gag cag	1459
	Met Lys Leu Glu Ala Glu Ile Glu Asn Thr Lys Leu Ala Lys Glu Gln	
	440 445 450	
	gcc att gga act caa gaa tac gaa aaa gct gca ggt tta cgt gat gaa	1507
	Ala Ile Gly Thr Gln Glu Tyr Glu Lys Ala Ala Gly Leu Arg Asp Glu	
	455 460 465	
50	gag aaa aaa ctt cgc gaa cgt ctg caa agt atg aaa cag gaa tgg gaa	1555
	Glu Lys Lys Leu Arg Glu Arg Leu Gln Ser Met Lys Gln Glu Trp Glu	
	470 475 480 485	
	aat cat aaa gaa gag cac caa gtt cct gta gat gaa gaa gca gtc gct	1603
	Asn His Lys Glu Glu His Gln Val Pro Val Asp Glu Glu Ala Val Ala	
	490 495 500	
60	cag gta gtt tct cta caa aca gga att ccc tca gca agg ctc aca gaa	1651
	Gln Val Val Ser Leu Gln Thr Gly Ile Pro Ser Ala Arg Leu Thr Glu	
	505 510 515	

		gct gaa agt gag aag ctt ctg aag tta gaa gac acg tta aga aga aaa	1699
		Ala Glu Ser Glu Lys Leu Leu Lys Leu Glu Asp Thr Leu Arg Arg Lys	
		520 525 530	
		gtc att ggt caa aat gat gcc gtt acc agc att tgc cgt gcc atc cga	1747
		Val Ile Gly Gln Asn Asp Ala Val Thr Ser Ile Cys Arg Ala Ile Arg	
		535 540 545	
10		cgt tct cga aca ggg atc aaa gat cct aac cga cct acg ggc tcc ttc	1795
		Arg Ser Arg Thr Gly Ile Lys Asp Pro Asn Arg Pro Thr Gly Ser Phe	
		550 555 560 565	
		cta ttc ctt ggg cct acc ggt gta ggg aaa agc ctg ctc gcc caa caa	1843
		Leu Phe Leu Gly Pro Thr Gly Val Gly Lys Ser Leu Leu Ala Gln Gln	
		570 575 580	
20		att gct ata gag atg ttc ggt ggt gaa gac gct ctg att cag gta gac	1891
		Ile Ala Ile Glu Met Phe Gly Gly Glu Asp Ala Leu Ile Gln Val Asp	
		585 590 595	
		atg tca gag tac atg gag aaa ttt gct gct acc aag atg atg gga tca	1939
		Met Ser Glu Tyr Met Glu Lys Phe Ala Ala Thr Lys Met Met Gly Ser	
		600 605 610	
		cct cca gga tat gta ggt cat gaa gaa ggg ggc cac ctt acg gaa cag	1987
		Pro Pro Gly Tyr Val Gly His Glu Glu Gly Gly His Leu Thr Glu Gln	
		615 620 625	
30		gta cgt cgc cgt cct tac tgc gtt gtt ctc ttt gat gag ata gaa aag	2035
		Val Arg Arg Arg Pro Tyr Cys Val Val Leu Phe Asp Glu Ile Glu Lys	
		630 635 640 645	
		gca cac cca gac att atg gac ctg atg ttg caa att tta gag caa gga	2083
		Ala His Pro Asp Ile Met Asp Leu Met Leu Gln Ile Leu Glu Gln Gly	
		650 655 660	
40		cgt ctt act gat tct ttt ggt cgc aaa gtg gat ttc cgt cat gcc att	2131
		Arg Leu Thr Asp Ser Phe Gly Arg Lys Val Asp Phe Arg His Ala Ile	
		665 670 675	
		att atc atg acc tcc aat ttg gga gct gat ctc att cgt aaa agc gga	2179
		Ile Ile Met Thr Ser Asn Leu Gly Ala Asp Leu Ile Arg Lys Ser Gly	
		680 685 690	
		gaa att ggt ttt ggc ttg aag tcc cat atg gac tat aag gtc atc caa	2227
		Glu Ile Gly Phe Gly Leu Lys Ser His Met Asp Tyr Lys Val Ile Gln	
		695 700 705	
50		gag aaa atc gaa cat gct atg aag aaa cac tta aag cct gag ttc att	2275
		Glu Lys Ile Glu His Ala Met Lys Lys His Leu Lys Pro Glu Phe Ile	
		710 715 720 725	
		aac cgt ttg gat gaa agt gtg att ttc cgt ccc ctc gag aaa gaa tct	2323
		Asn Arg Leu Asp Glu Ser Val Ile Phe Arg Pro Leu Glu Lys Glu Ser	
		730 735 740	
60		cta tcg gag atc atc cat tta gag atc aac aaa ctg gac tcg aga ctg	2371
		Leu Ser Glu Ile Ile His Leu Glu Ile Asn Lys Leu Asp Ser Arg Leu	
		745 750 755	

aaa aac tac caa atg gct ttg aac atc cca gac tct gtg att tcc ttc 2419  
 Lys Asn Tyr Gln Met Ala Leu Asn Ile Pro Asp Ser Val Ile Ser Phe  
 760 765 770

cta gta acg aag ggg cat tct cca gaa atg gga gca cgt cct cta cgc 2467  
 Leu Val Thr Lys Gly His Ser Pro Glu Met Gly Ala Arg Pro Leu Arg  
 775 780 785

10

cgt gtc att gag cag tac ctt gaa gat cct cta gcg gag ctc ttg ctt 2515  
 Arg Val Ile Glu Gln Tyr Leu Glu Asp Pro Leu Ala Glu Leu Leu Leu  
 790 795 800 805

aaa gag tcc tgc cgt caa gaa gct cgc aag cta cga gca acc ttg gtt 2563  
 Lys Glu Ser Cys Arg Gln Glu Ala Arg Lys Leu Arg Ala Thr Leu Val  
 810 815 820

gaa aat cgc gtt gcc ttt gaa agg gaa gaa gag gag cag gaa gct gct 2611  
 20 Glu Asn Arg Val Ala Phe Glu Arg Glu Glu Glu Glu Gln Glu Ala Ala  
 825 830 835

ctc cct agc cct cac ttg gaa tca taggaacgctc gataactcca ctaccaaggc 2665  
 Leu Pro Ser Pro His Leu Glu Ser  
 840 845

aggtatctcc ttgataaaac gctattgttt gtccctggagt taccgccttg acggggttg 2725  
 aaaatcgcac ctt 2738

30

<210> 18  
 <211> 845  
 <212> PRT  
 <213> Chlamydia pneumoniae

<220>  
 <221> SITE  
 <222> (467)...(492)  
 <223> B-cell epitope

40

<220>  
 <221> SITE  
 <222> (548)...(563)  
 <223> B-cell epitope

<220>  
 <221> SITE  
 <222> (565)...(574)  
 <223> T-cell epitope

50

<220>  
 <221> SITE  
 <222> (410)...(418)  
 <223> T-cell epitope

<400> 18  
 Met Phe Glu Lys Phe Thr Asn Arg Ala Lys Gln Val Ile Lys Leu Ala  
 1 5 10 15

60

Lys Lys Glu Ala Gln Arg Leu Asn His Asn Tyr Leu Gly Thr Glu His  
 20 25 30

Ile Leu Leu Gly Leu Leu Lys Leu Gly Gln Gly Val Ala Val Asn Val  
                   35                                  40                                  45  
 Leu Arg Asn Leu Gly Ile Asp Phe Asp Thr Ala Arg Gln Glu Val Glu  
           50                                  55                                  60  
 10 Arg Leu Ile Gly Tyr Gly Pro Glu Ile Gln Val Tyr Gly Asp Pro Ala  
       65                                  70                                  75                                  80  
 Leu Thr Gly Arg Val Lys Lys Ser Phe Glu Ser Ala Asn Glu Glu Ala  
                   85                                  90                                  95  
 Ser Leu Leu Glu His Asn Tyr Val Gly Thr Glu His Leu Leu Leu Gly  
                   100                                  105                                  110  
 20 Ile Leu His Gln Ser Asp Ser Val Ala Leu Gln Val Leu Glu Asn Leu  
           115                                  120                                  125  
 His Ile Asp Pro Arg Glu Val Arg Lys Glu Ile Leu Arg Glu Leu Glu  
       130                                  135                                  140  
 Thr Phe Asn Leu Gln Leu Pro Pro Ser Ser Ser Ser Ser Ser Ser Ser  
       145                                  150                                  155                                  160  
 Ser Arg Ser Asn Pro Ser Ser Ser Lys Ser Pro Leu Gly His Ser Leu  
                   165                                  170                                  175  
 30 Gly Ser Asp Lys Asn Glu Lys Leu Ser Ala Leu Lys Ala Tyr Gly Tyr  
           180                                  185                                  190  
 Asp Leu Thr Glu Met Val Arg Glu Ser Lys Leu Asp Pro Val Ile Gly  
           195                                  200                                  205  
 Arg Ser Ser Glu Val Glu Arg Leu Ile Leu Ile Leu Cys Arg Arg Arg  
       210                                  215                                  220  
 40 Lys Asn Asn Pro Val Leu Ile Gly Glu Ala Gly Val Gly Lys Thr Ala  
       225                                  230                                  235                                  240  
 Ile Val Glu Gly Leu Ala Gln Lys Ile Ile Leu Asn Glu Val Pro Asp  
           245                                  250                                  255  
 Ala Leu Arg Lys Lys Arg Leu Ile Thr Leu Asp Leu Ala Leu Met Ile  
           260                                  265                                  270  
 50 Ala Gly Thr Lys Tyr Arg Gly Gln Phe Glu Glu Arg Ile Lys Ala Val  
           275                                  280                                  285  
 Met Asp Glu Val Arg Lys His Gly Asn Ile Leu Leu Phe Ile Asp Glu  
       290                                  295                                  300  
 Leu His Thr Ile Val Gly Ala Gly Ala Ala Glu Gly Ala Ile Asp Ala  
       305                                  310                                  315                                  320  
 Ser Asn Ile Leu Lys Pro Ala Leu Ala Arg Gly Glu Ile Gln Cys Ile  
           325                                  330                                  335  
 60 Gly Ala Thr Thr Ile Asp Glu Tyr Arg Lys His Ile Glu Lys Asp Ala  
           340                                  345                                  350



Ala Leu Glu Arg Arg Phe Gln Lys Ile Val Val His Pro Pro Ser Val  
                   355                                  360                                  365

Asp Glu Thr Ile Glu Ile Leu Arg Gly Leu Lys Lys Lys Tyr Glu Glu  
           370                                  375                                  380

10 His His Asn Val Phe Ile Thr Glu Glu Ala Leu Lys Ala Ala Ala Thr  
    385                                  390                                  395                                  400

Leu Ser Asp Gln Tyr Val His Gly Arg Phe Leu Pro Asp Lys Ala Ile  
                                   405                                  410                                  415

Asp Leu Leu Asp Glu Ala Gly Ala Arg Val Arg Val Asn Thr Met Gly  
                                   420                                  425                                  430

20 Gln Pro Thr Asp Leu Met Lys Leu Glu Ala Glu Ile Glu Asn Thr Lys  
                                   435                                  440                                  445

Leu Ala Lys Glu Gln Ala Ile Gly Thr Gln Glu Tyr Glu Lys Ala Ala  
           450                                  455                                  460

Gly Leu Arg Asp Glu Glu Lys Lys Leu Arg Glu Arg Leu Gln Ser Met  
    465                                  470                                  475                                  480

Lys Gln Glu Trp Glu Asn His Lys Glu Glu His Gln Val Pro Val Asp  
                                   485                                  490                                  495

30 Glu Glu Ala Val Ala Gln Val Val Ser Leu Gln Thr Gly Ile Pro Ser  
                                   500                                  505                                  510

Ala Arg Leu Thr Glu Ala Glu Ser Glu Lys Leu Leu Lys Leu Glu Asp  
                                   515                                  520                                  525

Thr Leu Arg Arg Lys Val Ile Gly Gln Asn Asp Ala Val Thr Ser Ile  
    530                                  535                                  540

40 Cys Arg Ala Ile Arg Arg Ser Arg Thr Gly Ile Lys Asp Pro Asn Arg  
    545                                  550                                  555                                  560

Pro Thr Gly Ser Phe Leu Phe Leu Gly Pro Thr Gly Val Gly Lys Ser  
                                   565                                  570                                  575

Leu Leu Ala Gln Gln Ile Ala Ile Glu Met Phe Gly Gly Glu Asp Ala  
                                   580                                  585                                  590

50 Leu Ile Gln Val Asp Met Ser Glu Tyr Met Glu Lys Phe Ala Ala Thr  
                                   595                                  600                                  605

Lys Met Met Gly Ser Pro Pro Gly Tyr Val Gly His Glu Glu Gly Gly  
           610                                  615                                  620

His Leu Thr Glu Gln Val Arg Arg Arg Pro Tyr Cys Val Val Leu Phe  
    625                                  630                                  635                                  640

Asp Glu Ile Glu Lys Ala His Pro Asp Ile Met Asp Leu Met Leu Gln  
                                   645                                  650                                  655

60 Ile Leu Glu Gln Gly Arg Leu Thr Asp Ser Phe Gly Arg Lys Val Asp  
                                   660                                  665                                  670

	Phe Arg His Ala Ile Ile Ile Met Thr Ser Asn Leu Gly Ala Asp Leu	
	675	680 685
	Ile Arg Lys Ser Gly Glu Ile Gly Phe Gly Leu Lys Ser His Met Asp	
	690	695 700
10	Tyr Lys Val Ile Gln Glu Lys Ile Glu His Ala Met Lys Lys His Leu	
	705	710 715 720
	Lys Pro Glu Phe Ile Asn Arg Leu Asp Glu Ser Val Ile Phe Arg Pro	
	725	730 735
	Leu Glu Lys Glu Ser Leu Ser Glu Ile Ile His Leu Glu Ile Asn Lys	
	740	745 750
	Leu Asp Ser Arg Leu Lys Asn Tyr Gln Met Ala Leu Asn Ile Pro Asp	
20	755	760 765
	Ser Val Ile Ser Phe Leu Val Thr Lys Gly His Ser Pro Glu Met Gly	
	770	775 780
	Ala Arg Pro Leu Arg Arg Val Ile Glu Gln Tyr Leu Glu Asp Pro Leu	
	785	790 795 800
	Ala Glu Leu Leu Leu Lys Glu Ser Cys Arg Gln Glu Ala Arg Lys Leu	
	805	810 815
30	Arg Ala Thr Leu Val Glu Asn Arg Val Ala Phe Glu Arg Glu Glu Glu	
	820	825 830
	Glu Gln Glu Ala Ala Leu Pro Ser Pro His Leu Glu Ser	
	835	840 845
	<210> 19	
	<211> 509	
	<212> DNA	
40	<213> Chlamydia pneumoniae	
	<220>	
	<221> CDS	
	<222> (101)..(406)	
	<400> 19	
	gattcagggtt ctagtgagct tatgctcatg gaagttcaag tcttcttagc tgcaagaaaa	60
	taacaggggac agtaattcga tttttcgaga agggaaactt atg gta aag atc ata	115
50	Met Val Lys Ile Ile	
	1 5	
	tca agt gaa aat ttt gac tct ttt att gca tcg ggg ctg gtt ctg gtt	163
	Ser Ser Glu Asn Phe Asp Ser Phe Ile Ala Ser Gly Leu Val Leu Val	
	10 15 20	
	gat ttc ttt gca gaa tgg tgt ggc ccc tgt cgg atg ctg act cct atc	211
	Asp Phe Phe Ala Glu Trp Cys Gly Pro Cys Arg Met Leu Thr Pro Ile	
	25 30 35	
60		

tta gaa aat ctt gct gcg gaa ctt cct cat gtc act att gga aaa atc 259  
 Leu Glu Asn Leu Ala Ala Glu Leu Pro His Val Thr Ile Gly Lys Ile  
           40                          45                          50

aat ata gat gag aac agc aag cct gca gaa acg tac gaa gtc agc tct 307  
 Asn Ile Asp Glu Asn Ser Lys Pro Ala Glu Thr Tyr Glu Val Ser Ser  
           55                          60                          65

10 att cct acg ctt att ctt ttt aag gat ggg aac gag gtg gct cgg gtc 355  
 Ile Pro Thr Leu Ile Leu Phe Lys Asp Gly Asn Glu Val Ala Arg Val  
           70                          75                          80                          85

gta ggt ctt aag gat aaa gaa ttc cta acc aat ctt atc aat aag cac 403  
 Val Gly Leu Lys Asp Lys Glu Phe Leu Thr Asn Leu Ile Asn Lys His  
                           90                          95                          100

gct taaaaagacg ctgcaatatt aaaccgtagg attcttttgc aatgctacgg 456  
 20 Ala

ttttctgcct taccacttca tataaaacga tccctacact ggtagctaaa ttt 509

<210> 20  
 <211> 102  
 <212> PRT  
 <213> Chlamydia pneumoniae

30 <220>  
     <221> SITE  
     <222> (543)...(66)  
     <223> B-cell epitope

    <220>  
     <221> SITE  
     <222> (40)...(48)  
     <223> T-cell epitope

40 <220>  
     <221> SITE  
     <222> (74)...(83)  
     <223> T-cell epitope

<400> 20  
 Met Val Lys Ile Ile Ser Ser Glu Asn Phe Asp Ser Phe Ile Ala Ser  
       1                          5                          10                          15

Gly Leu Val Leu Val Asp Phe Phe Ala Glu Trp Cys Gly Pro Cys Arg  
 50                   20                          25                          30

Met Leu Thr Pro Ile Leu Glu Asn Leu Ala Ala Glu Leu Pro His Val  
       35                          40                          45

Thr Ile Gly Lys Ile Asn Ile Asp Glu Asn Ser Lys Pro Ala Glu Thr  
       50                          55                          60

Tyr Glu Val Ser Ser Ile Pro Thr Leu Ile Leu Phe Lys Asp Gly Asn  
       65                          70                          75                          80

60

Glu Val Ala Arg Val Val Gly Leu Lys Asp Lys Glu Phe Leu Thr Asn  
85 90 95

Leu Ile Asn Lys His Ala  
100

```

10      <210> 21
        <211> 43
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> 5' PCR primer

        <400> 21
        ataagaatgc ggccgccacc atgaagatgc ataggcttaa acc          43

20

        <210> 22
        <211> 36
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> 3' PCR primer

30      <400> 22
        gcgccggtatc ccacttaaga tatcgatatt tttag          36

        <210> 23
        <211> 45
        <212> DNA
        <213> Artificial Sequence

        <220>
40      <223> 5' PCR primer

        <400> 23
        ataagaatgc ggccgccacc atgcggttgg gaaataagcc tatgc          45

        <210> 24
        <211> 35
        <212> DNA
        <213> Artificial Sequence

50      <220>
        <223> 3' PCR primer

        <400> 24
        gcgccggtac cgtaatttaa tactctttga agggc          35

        <210> 25
        <211> 49
60      <212> DNA
        <213> Artificial Sequence

```

<220>  
<223> 5' PCR primer

<400> 25  
ataagaatgc ggccgccacc atgctcacc taggcttgga aagttcttg 49

10 <210> 26  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 3' PCR primer

<400> 26  
gctttggagg atccccggag aggctaagga gaatgg 36

20 <210> 27  
<211> 44  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 5' PCR primer

30 <400> 27  
ataagaatgc ggccgccacc atgaaaaaag ggaaattagg agcc 44

<210> 28  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
40 <223> 3' PCR primer

<400> 28  
gcgcggatc cccgaagcag aagtcgttgt ggg 33

<210> 29  
<211> 48  
<212> DNA  
<213> Artificial Sequence

50 <220>  
<223> 5' PCR primer

<400> 29  
ataagaatgc ggccgccacc atgagaaaac ttattttatg caatccta 48

<210> 30  
<211> 33  
60 <212> DNA  
<213> Artificial Sequence

<220>  
<223> 3' PCR primer

<400> 30  
gcgccggatc ccagaacaac ggagttcttt tgg 33

10 <210> 31  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 5' PCR primer

<400> 31  
ataagaatgc ggccgccacc atgaataaaa aaaatctaac tatttg 46

20 <210> 32  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 3' PCR primer

30 <400> 32  
gcgccggatc ccagcgatag cttctggggt cc 32

<210> 33  
<211> 42  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 5' PCR primer

40 <400> 33  
ataagaatgc ggccgccacc atgacactgg taccctatgt tg 42

<210> 34  
<211> 35  
<212> DNA  
<213> Artificial Sequence

50 <220>  
<223> 3' PCR primer

<400> 34  
gcgccggatc ccagtgtac ttgtatcctt attag 35

<210> 35  
<211> 45  
<212> DNA  
<213> Artificial Sequence

60

<220>  
<223> 5' PCR primer

<400> 35  
ataagaatgc ggccgccacc atgagctacc gtaaactgtc gactc 45

10 <210> 36  
<211> 35  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 3' PCR primer

<400> 36  
gcgcgggac cccctcggtc ccccttggtt cggag 35

20 <210> 37  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 5' PCR primer

30 <400> 37  
ataagaatgc ggccgccacc atgtttgaga agttcactaa tagagc 46

<210> 38  
<211> 34  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 3' PCR primer

40 <400> 38  
gcgcgggtac cgtgattcca atgaggggt aggg 34

<210> 39  
<211> 42  
<212> DNA  
<213> Artificial Sequence

50 <220>  
<223> 5' PCR primer

<400> 39  
ataagaatgc ggccgccacc atggtaaaga tcatatcaag tg 42

<210> 40  
<211> 30  
<212> DNA  
<213> Artificial Sequence

60

<220>  
 <223> 3' PCR primer  
  
 <400> 40  
 gcgccggatc ccagcgtgct tattgataag 30

10 <210> 41  
 <211> 17  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> B-cell epitope of ATP-binding cassette protein  
  
 <400> 41  
 Val His His Thr Leu Arg Glu Ser Tyr Lys Lys Gly Thr Pro Pro  
 20 1 5 10 15  
 Ser Thr  
  
 <210> 42  
 <211> 16  
  
 <212> PRT  
 <213> Artificial Sequence  
 30  
 <220>  
 <223> B-cell epitope of ATP-binding cassette protein  
  
 <400> 42  
 Asn Leu Gln Lys Glu Ile Ser Thr Glu Glu Arg Gln Thr Lys Ala  
 1 5 10 15  
 Arg  
  
 40  
 <210> 43  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 <223> T-cell epitope of ATP-binding cassette protein  
  
 <400> 43  
 50 Trp Ile Ala Glu Tyr Val Ser Pro Val  
 1 5  
  
 <210> 44  
 <211> 12  
 <212> PRT  
 <213> Artificial Sequence  
  
 <220>  
 60 <223> B-cell epitope of endopeptidase protein



<400> 44  
 Lys Gly Asn Asn Ser Ser Pro Arg Ser Pro Ala Pro  
     1                    5                    10

<210> 45  
 <211> 9  
 <212> PRT  
 10 <213> Artificial Sequence

<220>  
 <223> B-cell epitope of endopeptidase protein

<400> 45  
 Gly Glu Asn Phe Gln Lys Asn Ser Ser  
     1                    5

20 <210> 46  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> T-cell epitope of endopeptidase protein

<400> 46  
 Leu Leu Ile Glu Asp Met Asp Leu Ile  
 30     1                    5

<210> 47  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> T-cell epitope of endopeptidase protein

40 <400> 47  
 Asn Leu Leu Ile Glu Asp Met Asp Leu  
     1                    5

<210> 48  
 <211> 16  
 <212> PRT  
 <213> Artificial Sequence

50 <220>  
 <223> B-cell epitope of protease protein

<400> 48  
 Thr Asp Leu Glu Gly Leu Glu Glu Asp His Lys Asp Ser Pro Trp  
     1                    5                    10                    15

Glu

60

<210> 49  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> B-cell epitope of protease protein

10 <400> 49  
Ser Glu Asn Ala Lys Lys Ser Glu Glu Gln Thr Ser Pro Gln Glu  
1 5 10 15  
Thr Pro Glu

<210> 50  
<211> 9  
20 <212> PRT  
<213> Artificial Sequence

<220>  
<223> T-cell epitope of protease protein

<400> 50  
Tyr Leu Gly Asp Glu Ile Leu Glu Val  
1 5

30 <210> 51  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> T-cell epitope of protease protein

<400> 51  
40 Tyr Leu Tyr Ser Leu Leu Ser Met Leu  
1 5

<210> 52  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
50 <223> B-cell epitope of metalloprotease protein

<400> 52  
Thr Thr Asn Arg Gln Lys Ala Leu  
1 5

<210> 53  
<211> 11  
<212> PRT  
60 <213> Artificial Sequence

<220>  
<223> B-cell epitope of metalloprotease protein

<400> 53  
Val Asn Ser Ser Asn Ser Asn Arg Leu Arg Glu  
1 5 10

10 <210> 54  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> T-cell epitope of metalloprotease protein

<400> 54  
20 Ser Val Leu Ser Arg Val Asn Tyr Val  
1 5

<210> 55  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
30 <223> T-cell epitope of metalloprotease protein

<400> 55  
Lys Leu Ser Ser Leu Ile Pro Gly Leu  
1 5

<210> 56  
<211> 9  
<212> PRT  
40 <213> Artificial Sequence

<220>  
<223> T-cell epitope of metalloprotease protein

<400> 56  
Ile Leu Ile Gly His Lys Lys His Val  
1 5

50 <210> 57  
<211> 14  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> B-cell epitope of CLP protease ATPase protein

<400> 57  
Pro Pro Lys Gly Gly Arg Lys His Pro Asn Gln Glu Tyr Ile  
60 5 10

<210> 58  
<211> 14  
<212> PRT  
<213> Artificial Sequence

10 <220>  
<223> B-cell epitope of CLP protease ATPase protein

<400> 58  
Ser Asp Asp Gln Ala Asp Leu Ser Gln Lys Thr Arg Asp His  
1 5 10

<210> 59  
<211> 9  
<212> PRT  
<213> Artificial Sequence

20 <220>  
<223> T-cell epitope of CLP protease ATPase protein

<400> 59  
Lys Ile Leu Asp Val Pro Phe Thr Ile  
1 5

30 <210> 60  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> T-cell epitope of CLP protease ATPase protein

<400> 60  
Leu Leu Gln Ala Ala Asp Tyr Asp Val  
1 5

40 <210> 61  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> B-cell epitope of CLP protease subunit protein

50 <400> 61  
Gly Thr Lys Gly Lys Arg His Ala Leu  
1 5

<210> 62  
<211> 11  
<212> PRT  
<213> Artificial Sequence

60 <220>  
<223> B-cell epitope of CLP protease subunit protein

<400> 62  
Ala Lys Glu Thr Asn Lys Asp Thr Ser Ser Thr  
1 5 10

<210> 63  
<211> 9  
10 <212> PRT  
<213> Artificial Sequence

<220>  
<223> T-cell epitope of CLP protease subunit protein

<400> 63  
Ala Ile Tyr Asp Thr Ile Arg Phe Leu  
1 5

20 <210> 64  
<211> 19  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> B-cell epitope of translycolase/transpeptidase protein

<400> 64  
30 Asp Pro Thr Asn Tyr Lys Glu Tyr Phe Asn Asn Lys Glu Arg Ile  
1 5 10 15

Glu His Thr Lys

<210> 65  
<211> 17  
<212> PRT  
<213> Artificial Sequence

40 <220>  
<223> B-cell epitope of translycolase/transpeptidase protein

<400> 65  
Lys Arg Leu Tyr Glu Glu Trp Asn Arg Ser Pro Lys Gln Gly Gly  
1 5 10 15

Thr Arg

50 <210> 66  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> T-cell epitope of translycolase/transpeptidase protein

<400> 66  
60 Ala Leu Gly Gln His Glu Phe Cys Val  
1 5

<210> 67  
<211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> T-cell epitope of translycolase/transpeptidase protein

10 <400> 67  
Ile Leu Ala Thr Gly Ile Gln Met Val  
1 5

<210> 68  
<211> 26  
<212> PRT  
<213> Artificial Sequence

20 <220>  
<223> B-cell epitope of CLPc protease protein

<400> 68  
Arg Asp Glu Glu Lys Lys Leu Arg Glu Arg Leu Gln Ser Met Lys  
1 5 10 15  
Gln Glu Trp Glu Asn His Lys Glu Glu His Gln  
20 25

30 <210> 69  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> B-cell epitope of CLPc protease protein

40 <400> 69  
Ile Arg Arg Ser Arg Thr Gly Ile Lys Asp Pro Asn Arg Pro Thr  
1 5 10 15  
Gly

<210> 70  
<211> 9  
<212> PRT  
50 <213> Artificial Sequence

<220>  
<223> T-cell epitope of CLPc protease protein

<400> 70  
Phe Leu Phe Leu Gly Pro Thr Gly Val  
1 5

60 <210> 71  
<211> 9

<212> PRT  
<213> Artificial Sequence

<220>  
<223> T-cell epitope of CLPc protease protein

<400> 71  
10 Phe Leu Pro Asp Lys Ala Ile Asp Leu  
1 5

<210> 72  
<211> 13  
<212> PRT  
<213> Artificial Sequence

<220>  
20 <223> B-cell epitope of thioredoxin

<400> 72  
Asn Ile Asp Glu Asn Ser Lys Pro Ala Glu Thr Tyr Glu  
1 5 10

<210> 73  
<211> 9  
<212> PRT  
30 <213> Artificial Sequence

<220>  
<223> B-cell epitope of thioredoxin

<400> 73  
Asn Leu Ala Ala Glu Leu Pro His Val  
1 5

<210> 74  
40 <211> 9  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> T-cell epitope of thioredoxin

<400> 74  
50 Ile Leu Phe Lys Asp Gly Asn Glu Val  
1 5